OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.3
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Run on: October 19, 2002, 07:52:31 ; Search time 1919 Seconds
(without alignments)
4994.452 Million cell updates/sec

Title:
Perfect score: 2359
Sequence: 1 MAPSDSVGDVTKILAASES...........DPSKALIRKVSTEADNLLEK 458

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext   0.5
Ygapop 10.0 , Ygapext   0.5
Fgapop   6.0 , Fgapext   7.0
Delop   6.0 , Delext   7.0

Searched: 1797656 seqs, 1046326893 residues

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Command line parameters:
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-Q=/cgn2_1/USPTO.spool/US09807459/runat_18102002_141112_28581/app_query.fasta_1.647
-DB=GenEmbl -QFMT=fastp -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
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29:   em_vi:*
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31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2359	100.0	1810	3	AB017700	Babesia c
2	2355	99.8	1943	3	AF092736	Babesia c
3	996.5	42.2	1542	6	A16430	(Lambda EMB
4	831.5	35.2	2089	3	AF030060	Babesia b
5	831.5	35.2	2089	3	AF030058	Babesia b
6	830.5	35.2	2323	3	AF030061	Babesia b
7	827.5	35.1	1962	6	M60878	B.bigemina
8	827.5	35.1	1962	3	I12361	Sequence 3
9	826.5	35.0	1962	3	M85186	Babesia big
10	826.5	35.0	1990	3	M38218	Babesia bov
11	826.5	35.0	2087	3	AF030057	Babesia b
12	826.5	35.0	2089	3	AF030053	Babesia b
13	826.5	35.0	2089	3	AF030054	Babesia b
14	826.5	35.0	2089	3	AF030055	Babesia b
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16	826.5	35.0	2325	3	AF030056	Babesia b
17	825.5	35.0	11184	3	AF027149	Babesia b
18	825.5	35.0	2325	3	AF030062	Babesia b
19	823	34.9	2005	3	BBODNAA	Babesia
20	813.5	34.5	1962	3	BBODNAD	Babesia
21	790	33.5	2005	3	BBODNAB	Babesia
22	770.5	32.7	1371	6	A16434	(Lambda GEM
23	770.5	32.7	2796	3	BBORHOPCN	Babesia
24	759.5	32.2	1491	6	A16432	(Lambda EMB
25	759.5	32.2	4145	3	BBORHOP2OV	Babesia
26	665.5	28.2	2549	3	BBORA1P	Babesia
27	632.5	26.8	2851	3	BBORHP2340	Babesia
28	569.5	24.1	4414	3	Z49818	B.divergens
29	555	23.5	4414	3	BDRHASPR	Babesia
30	532	22.6	575	3	AF026272	Babesia
31	532	22.6	575	3	AF014757	Babesia
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33	532	22.6	575	3	AF014760	Babesia
34	532	22.6	575	3	AF014768	Babesia
35	527	22.3	575	3	AF014761	Babesia
36	527	22.3	575	3	AF014764	Babesia
37	520	22.0	574	3	AF014767	Babesia
38	520	22.0	823	3	AF014759	Babesia
39	513	21.7	575	3	AF014763	Babesia
40	513	21.7	866	3	AF014765	Babesia
41	476	20.2	670	3	AF092735	Babesia c
42	449	19.0	508	3	AF014766	Babesia c
43	442.5	18.8	1016	3	AF017297	Babesia b
44	441.5	18.7	1016	3	AF017296	Babesia b
45	440.5	18.7	1016	3	AF017295	Babesia b

ALIGNMENTS

RESULT 1
AB017700
LOCUS   AB017700   1810 bp   mRNA   linear   INV 11-DEC-1999
DEFINITION   Babesia caballi pBC48/31 mRNA for 48KDa merozoite antigen, complete
cds.
ACCESSION   AB017700
VERSION   AB017700.1   GI:5821173
KEYWORDS   48kDa merozoite antigen; BC48/31.
SOURCE   Babesia caballi (strain:USDA) cDNA to mRNA.

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ORGANISM   Babesia caballi
           Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
           Babesia.
REFERENCE  1 (sites)
AUTHORS    Ikadai,H., Xuan,X., Igarashi,I., Tanaka,S., Kanemaru,T.,
           Nagasawa,H., Fujisaki,K., Suzuki,N. and Mikami,T.
TITLE      Cloning and expression of a 48-kilodalton babesia caballi merozoite
           rhoptry protein and potential use of the recombinant antigen in an
           enzyme-linked immunosorbent assay
JOURNAL    J. Clin. Microbiol. 37 (11), 3475-3480 (1999)
MEDLINE    99454831
REFERENCE  2 (bases 1 to 1810)
AUTHORS    Ikadai,H., Xuan,X., Igarashi,I., Tanaka,T., Abgaandorjiin,A.,
           Inoue,N., Nagasawa,H., Fujisaki,K., Mikami,T., Toyoda,Y. and
           Suzuki,N.
TITLE      Direct Submission
JOURNAL    Submitted (16-SEP-1998) Hiromi Ikadai, Obihiro University of
           Agriculture and Veterinary Medicine, The Research Center for
           Protozoan Molecular Immunology; Inadacho Nishi 2 Sen 13, Obihiro,
           Hokkaido 080-8555, Japan (E-mail:d09013@obihiro.ac.jp,
           Tel:81-155-49-5647, Fax:81-155-49-5643)
FEATURES             Location/Qualifiers
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                     /strain="USDA"
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                     /note="18 a nucleotides"
BASE COUNT      505 a    412 c    460 g    433 t
ORIGIN
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US-09-807-459-2 (1-458) x AB017700 (1-1810)

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Score:                  2359.00             Matches:           458
Percent Similarity:     100.00%             Conservative:        0
Percent Identity:       100.00%             Mismatches:          0
Best Local Similarity:  100.00%             Indels:              0
Query Match:            100.00%             Gaps:                0
Db:                     3
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Db    39 ATGGCTCCCAGCGACTCTGTGGGCGACGTGACTAAGACCTTATTGGCTGCCAGCGAAAGT  98

Qy    21 ValAspSerAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla     40
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Qy    41 ValSerAspAsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSer   60
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Db   159 GTGTCTGACAACTTCGCCGAGCGCATTTGCAGTCAAGTCCCTAAGGGAGTAACTGCAGT  218

Qy    61 AlaSerValSerAlaValMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer   80
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Db   219 GCTTCCGTTAGCGCATACATGAGTCGCTGCGCTAAGCAGGACTGCCTGACTCTCCAAAGT 278

Qy    81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu  100
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Db   279 CTTAAGTACCCCCTCGAGGCTAAGTACCAGCCTCTCACGCTCCCTGACCCCTACCAGTTG 338

Qy   101 GluAlaAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys 120
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Db   339 GAGGCCGCCGCATTTATTACTTCTTCAAGGAGAGTGACGCTAATCCGGCCAATAGCACAGAG 398

Qy   121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe  140
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Db   399 CGCTTCTGGATGCGTTTCAGAAGGGGCAAGAACCACAGTTACTTCCACGACTTAGTCTTC 458

Qy   141 AsnLeuLeuGluLysAsnValThrArgAspAlaAspThrAspIleGluAsnPheAla    160
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Db   459 AATCTCCTGGAGAAGAACGTGACTCGCGACGCCGATACTGACATTGAGAACTTTGCG     518

Qy   161 SerArgTyrLeuTyrMetAlaThrLeuTyrLysThrTyrThrAsnValAspGluPhe    180
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Db   519 TCCAGGTACCTGTACATGGCCACGCTTTACTACACAAGACGTACAAATGTTGATGAGTTC 578

Qy   181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLys  200
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Qy   201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSer  220
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Db   639 AGGGCACTTAAGCAGATTATTCGCTCTAACCTGCCCCTTGACATCGGGACACAGAACAGC 698

Qy   221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspValMetAspThrGlnIlePro  240
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Db   699 GTCAGTCGCCTGCAGCACATTACGAGCAGTTACAAGGATGTCATGGACACCCAGATTCCT 758

Qy   241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr  260
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Qy   261 ValAlaGlyTyrValAspThrProTrpTyrLysLysTrpTyrMetLysLeuLysAsnPhe  280
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Db   879 ATGGTGAACAGGGTGTTCATTCCTTTCAAGAAGTTCTTCAATAAGGAAATTCGTGAGCCT 938

Qy   301 SerLysAlaLeuLysGluLysValSerThrAspThrLysAspLeuPheGluAsnLysIle  320
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Qy   321 GlyGlnGlyThrValAspPhePheAsnAsnGluIleArgAspProSerLysAlaLeuLys  340
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Db   999 GGGCAGGGTACTGTGGACTTTTCAATAAGGAAATTCGTGACCCTAGTAAGGCATTAAAA 1058

Qy   341 GluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrVal  360
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Db  1059 GAAAAAGTGTCAAACGACGCCAAGGATTTATTCGAGAACAAAATTGGGCAGGGTACTGTG 1118

Qy   361 AspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThr  380
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Db  1119 GACTTCATCAATAACGAAATTCGTGACCCTAGTAAGGCATTAATAAGGAAAGTGTCAACG 1178

Qy   381 GlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsn  400
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Qy   401 GluIleArgAspProSerLysAlaLeuIleArgLysValTyrThrGluAlaAspAspLeu  420
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Qy   421 PheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspPro  440
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Db  1299 TTCGAGAACAAAATTGGGCAGGGTACTGTGGACTTCATCAATAAGGAAATTCGTGACCCT 1358
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Qy    441 SerLysAlaLeuIleArgLysValSerThrGluAlaSerAspAsnLeuLeuGluLys 458
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Db   1359 AGTAAGGCATTAATAAGGAAAAGTGTCTACCGAGGCCGATAAATTTATTCGGAGAAA 1412
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RESULT 2

LOCUS   AF092736   1943 bp   mRNA   linear   INV 29-JUN-1999
DEFINITION   Babesia caballi clone x6 rhoptry-associated protein 1 (RAP-1) mRNA,
             complete cds.
ACCESSION   AF092736
VERSION   AF092736.1 GI:5230731
KEYWORDS   .
SOURCE   Babesia caballi.
  ORGANISM   Babesia caballi
             Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
             Babesia.
REFERENCE   1 (bases 1 to 1943)
  AUTHORS   Kappmeyer,L.S., Perryman,L.E., Hines,S.A., Baszler,T.V., Katz,J.B.,
             Hennager,S.G. and Knowles,D.P.
  TITLE   Detection of equine antibodies to babesia caballi by recombinant B.
             caballi rhoptry-associated protein 1 in a competitive-inhibition
             enzyme-linked immunosorbent assay
  JOURNAL   J. Clin. Microbiol. 37 (7), 2285-2290 (1999)
  MEDLINE   99294770
  PUBMED   10364599
REFERENCE   2 (bases 1 to 1943)
  AUTHORS   Kappmeyer,L.S. and Knowles,D.P.
  TITLE   Direct Submission
  JOURNAL   Submitted (18-SEP-1998) Agricultural Research Service, US
             Department of Agriculture, 337 Bustad Hall, Washington State
             University, Pullman, WA 99164-7030, USA
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BASE COUNT   528 a   438 c   498 g   479 t
ORIGIN

US-09-807-459-2 (1-458) x AF092736 (1-1943)

Alignment Scores:
Pred. No.:
Score: 2355.00
Percent Similarity: 99.78%
Best Local Similarity: 99.78%
Query Match: 99.83%
DB:

Length: 1943
Matches: 457
Conservative: 0
Mismatches: 1
Indels: 0
Gaps: 0.

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Db    209 ATGGCTCCCAGCGACTCTGTGGGCGACGTCACTAAGACCTTATTGGCTGCCAGCGAAAGT 268

Qy     21 ValAspSerAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla 40
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Qy     41 ValSerAspAsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSer 60
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Db    389 GCTTCCGTTAGCGCATAACATGAGTCGCTGGGCTAAACAGAGACTGCCTGACTCTCCAAAGT 448

Qy     61 AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
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Qy    101 GluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys 120
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Qy    121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
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Qy    161 SerArgTyrLeuMetAlaThrLeuTyrLysArgTyrThrAsnValAspGluPhe 180
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Qy    181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyGlyTrpGlyIleLys 200
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Qy    201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspGlyThrGluHisSer 220
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Db    809 AGGGCACTTAAGCAGATTATTCGCTCTAACCTGCCCCTTGACGGGACAGAACACAGC 868

Qy    221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro 240
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Db    869 GTCAGTCGCCTGCAGCACATTACGAGCAGTTACAAGGATTACATGGATACCCAGATTCCT 928

Qy    241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
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Db    929 GCACTGCCCAAGTTTGCGAAGCGTTTCTCCCTTATGGTAGTGCAGAGGCTGCTGGCCACC 988

Qy    261 ValAlaGlyTyrValAspPheTrpProTyrLysLysTrpMetLysLeuLysAsnPhe 280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    989 GTGGCCGGTTACGTCGACTTCTGGCCATATAAGAAGTGGATGAAGCTGAAGAACTTT 1048

Qy    281 MetValAsnArgValPheIleProThrIleLysLysPheAsnGluLysGluIleArgGluPro 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1049 ATGGTGAACAGGGTGTTCATTCCTACAAAGAAGTTCTTCAATAAGGAAAATCGTGAGCCT 1108

Qy    301 SerLysAlaLeuLysGluLysValSerThrAspThrLysAspLeuPheGluAsnLysIle 320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1109 AGTAAGGCATTAAAGGAGAAGGTGTCAACCGACACCAAGGATTTATTCGAGAACAAAATT 1168

Qy    321 GlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLys 340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1169 GGGCAGGGTACTGTGGACTTCTTCAATAAGGAAAATTCGTGACCCTAGTAAGGCATTAAA 1228

Qy    341 GluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleCysGlyGlnThrVal 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1229 GAAAAAGTGTCAAACGACGCCAAGGATTTATTCGAGAACAAAATTCGGCAGGGTACTGTG 1288

Qy    361 AspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThr 380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 GACTTCATCAATAACGAAAATTCGTGACCCTAGTAAGGCATTAATAAGGAAAAGTGTCAAC 1348

Qy    381 GlyAlaGluAspLeuPheGluAsnLysIleCysGlyGlnThrValAspPheIleAsnAsn 400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1349  GGGGCCGAGCGATTTATTCGAGAACAAAATTGGGCAGGGACTACTGTGGACTTCATCAATAAC      1408
Qy    401  GluIleLeuArgGlnAspProSerLysAlaLeuLeuLeuIleLeuArgLysValTyrThrGluAla  420
Db   1409  GAAATTCGTGCAACCTGTGAAGGCATTAATAAGAAAAGTGTACACCGAGGCCGATGATTTA       1468
Qy    421  PheGluAsnLysIleGlyIleThrValAspPheGluIleLeuArgAspPro               440
Db   1469  TTCGAGAACAAAATTGGGCAGGGACTACTGTGGACTTCATCAATAAGGAAAATTCGTGACCCT    1528
Qy    441  SerLysAlaLeuLeuIleLeuArgLysValSerThrGluAlaAspAsnLeuLeuGlyLys       458
Db   1529  AGTAAGGCAATTAATAAGAAAAAGTGTCTACCGAGGCCGATAATTTATTGGAGAAA           1582
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```
RESULT 3

LOCUS       A16430                  1542 bp    DNA     linear   PAT 23-MAR-1994
DEFINITION  (Lambda EMBL3 #5) genes 1-4 encoding 21B4/rhoptry homologues.
ACCESSION   A16430
VERSION     A16430.1  GI:511979
KEYWORDS    .
SOURCE      Babesia ovis
  ORGANISM  Babesia ovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 1542)
  AUTHORS   Babesia.
  TITLE     BABESIAL ANTIGENS
  JOURNAL   Patent: WO 9314204-A 8 22-JUL-1993;
FEATURES             Location/Qualifiers
     source          1..1542
                     /organism="Babesia ovis"
                     /db_xref="taxon:5869"
     CDS             1..1542
                     /codon_start=1
                     /product="21B4/rhoptry homologue"
                     /protein_id="CAA01283.1"
                     /db_xref="GI:511980"
                     /translation="MRAISSVVGCAFWLVAGSTVAIRHQQQAANLAPAEVVGNVAATL
                     STADIISHDYDKELINDMRDQMHREMGENFVDTVCTKAPEDSNGRQMVALYADRCEM
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                     KHGDYHRFIGLLALAKGVTRKDGADTDLEFLVNKLLYMATIYKYTLLIVNNSDAKFENRI
                     AFATKIFGFGIKALKDIVRSNVPEYMGEHSIERISHLAIGVKDIMLTQVPTLSKFAE
                     RYSDAVMKVLLSSLAGYVKAPWYKRWFNKVKDFYNKIGKPTKEHFHKKIHPRTAEFFD
                     KMHERTKDFFENKIGAPTKDFFENKIGAPTKDFFENKIGAPTKDFFENKIGAPTKDFF
                     ENKIGAPTKDFFENKIGAPTKDFFENKLPEHTKDFFENKLPEHTKDFFENKLPEHTKD
                     FFENKIGAPIKESEENLGIHKRPVNWRYISSPQRMNNDSVADVATETVDMENHDGGNTV
                     GEMPV"

BASE COUNT      455 a    366 c    343 g    378 t
ORIGIN
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```
US-09-807-459-2 (1-458) x A16430 (1-1542)

Alignment No.:
Pred. No.:               1.13e-71       Length:          1542
Score:                     996.50       Matches:          204
Percent Similarity:        62.64%       Conservative:      81
Best Local Similarity:     44.84%       Mismatches:       153
Query Match:               42.24%       Indels:            18
DB:                                     Gaps:               6
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```
Qy      1  MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer    20
           ::||||||:|| :|| | |:|
Db      1  CTAGCACCTCGTGAAGTAGTCGGTAATGTGGCCGCTACTTTGTCTACCGACGATGAGATT   150

Qy     21  ValAspSerSerAlaAlaAsnAlaTyrMetIleAsnSerArgAspMetSerAspTyrLeuSerAla   40
           ::|  |||
Db    151  ATATCATCACGACTATGATAAGGAGAGTTGTATAAATGATAGAGATCAGATGAGGGAA    210

Qy     41  ValSerAspAsnPheAlaGluArgIleCysSerSerGlnValProLeuGlySerAsnCysSer    60
           :||  |||
Db    211  ATGGGTGAGAACTTCGTTGACACCGTATGTCACGAAGGCCCCTGAGAATCCAACTGTCGC   270
```

```
Qy     61  AlaSerValSerAlaThrTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer    80
           |||||::  ||| :::|
Db    271  CAAATGGTTGCCCTCTTATGCTCAAGAGTCGTGGAGAGTGTGGTTGGTTGGGTTGCGGAACAAC  330

Qy     81  LeuLysTyrProLeuGlnAlaLysTyrGlnProLeuGluThrLeuProAlaProTyrGlnLeu   100
           :::|| ||||||||:::||||
Db    331  GTCAACTACCCCGTTGAGTGAGGAGAATACCAAACCCTTATCACTCCCCTACCCAATTG   390

Qy    101  GluIleAlaAlaPheIleLeuPheLysGluSerAlaAlaAsnProAlaAsnSerThrGluLys   120
           :||||||:||
Db    391  GATGCTGCCTTCACTTTGTTCAAGGAAACTGCGGCCAACCCTGCTAAAAGTACTGAAAAG   450

Qy    121  ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerThrTyrPheHisAspLeuValPhe   140
           |||:::|||  |:||||||  ::|
Db    451  GGTCAAATGGAATGGCGTTTCCGAAACGGGAAAAACCATGGTGACTACCACGGTTTCCTCATT   510

Qy    141  AsnLeuLeuGluLysAsnValThrArgAspAlaAlaThrAspIleThrAspLeuAsnPheAla   160
           |||  ||||||||:::  :::|||
Db    511  GGCTTGTTGGCAAAAGGCGTTACTCGTAAGGATGGTGCTACTGACCTTGAGTTCCTGGTC   570

Qy    161  SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysTyrThrArgAsnValAspGluPhe   180
           :::||| ||||||:: ::||| :||
Db    571  AACAAGCTTTTGTACATGGCCACCACCTATTACAAAACCTTAATTGTCAACAACAGC   630

Qy    181  GlyAlaSerPhePheAlaLysSerLeuSerPheThrThrGlyLeuPheGlyIleLys   200
           |||  :::  |||||||||  ::||
Db    631  GGTGCCAAATTCTTTAACAGGATTGCCCACGGTTACAAGGATGGTGCTACTGACCTCCA   690

Qy    201  ArgGlnAlaLeuLysGlnIleLeuIleArgSerAsnLeuProLeuAspIleGlyThrGlnHisSer   220
           ::||||  |||||||
Db    691  AAGGCCGCTCAAGGTAATGCTCCCCTCAATATGTCCCGAATATATGGGA---GAGCACAGT   747

Qy    221  ValSerArgGluGlnHisHisIleThrSerGluSerTyrTyrMetAspProThrGlnIlePro   240
           ::|  |::  ||:|
Db    748  ATTGAACGCATTAGTCATTTGGCCCACGGTTACAAGGACTACATGTTGACCCAAGTTCCA   807

Qy    241  AlaAlaLeuProLysSerPheAlaLysSerArgPheSerGluLeuMetValValGlnAsnArgLeuLeuAlaThr   260
           ::|  ||||||| ::||||||:::
Db    808  ACCCTTGCAAAGTTCGCCGAACGTTACTCTGACAAGGTTATGAAAGTTCTGTTGAGCAGC   867

Qy    261  ValAlaLeuGlyTyrValAspThrProTrpTyrLysTyrLysTyrMetLysLysLysAsnPhe   280
           :::|:||||||||||:::  ::|
Db    868  CTCGCCCGGTTATGTCAAGGCTCCATGGTATAAGGACTACAAGGTTAAAGATTTC   927

Qy    281  MetValAsnArgValPheIleProThrThrLysLysPhePheAsnLysIleGlyLysArgGluPro   300
           ||||||||||||||||||||||||||||||||||  :::|
Db    928  TTTGTTAACAAAATAGGCAAACCTACAAAGGAACACTTCCACAAG------AAACACCCA   981

Qy    301  SerLysAla---LeuLysGluLysValSerThrAspThrLysAspLeuPheGluAsnLys   319
           :: |||||||||||||||||||||||||||
Db    982  CGCACCGCCGCATTTTTCGACAAGATCGATGAACGCGAACGAGGACTTCTTCGAGAACAAG  1041

Qy    320  IleGlyIleGlyThrValAspPhePheAsnLysIleGlyIleGlyThrValAspPheIle   339
           |||||||||||||||||||:::  |||
Db   1042  ATAGGTGCTCCTACAAAGGACTTCTTCGAGAACAAGATAGGTGTTCCTACAAGGACTTC   1101

Qy    340  LysGlu----LysValSerAsnAspAlaLysPheGluAsnLysIleGlyIleGly   358
           |||||||||||||:::  |||
Db   1102  TTCGAGAACAAGATAGGTGCTCCTACCAAGGACTTCTTCGAGAACAAGATAGGTGCTCCT  1161

Qy    359  ThrValAspPheIleAsnAsnGluIleLeuArgGlnAspProSerLysAlaLeu   378
           ::||||||||||:: :||
Db   1162  ACCAAGGACTTCTTCGAGAACAAGATAGGTGCTCCTACCAAA------------------  1203

Qy    379  SerThrGlyAlaGluProPheGluAsnLysIleGlyIleGlyThrValAspPheIle   398
           ::|  :::  ||||||||||||:::|
Db   1204  ------------GACTTCTTCGAGAACAAGATAGGTGCTCCTACAAGGACTTC   1248

Qy    399  AsnAsnGluIleLeuArgAspProSerLysAlaLeuLeuIle---ArgLysValTyrThrGluAla   417
           |||  :::||||||
Db   1249  GACAACAAGCTCCTGAAGCACCACGGTTCTCCGAGAACAAGCACACACC  1308

Qy    418  AspAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIleAsnLysGluIle   437
```

```
RESULT 4

Db   1309 AAGGACTTCTTCGAGACAAGCAGCTGCCTGAACACCACCAAGGACTTCTTTGAGAACAAGATT 1368
          ||||||||||||||||||||:::|||        :::|                ::::||
Qy    438 ArgAspProSerLysAlaLeuIleArgValSerThrGluAla 452                      1368

Qy    438 ArgAspProSerLysAlaLeuIleArgLysValSerThrGluAla 452
          ||||                    ::::        |||::::||
Db   1369 GGTCGCCCCCATTAAGA-ATCATTTGAGAACTTGGGACACAAGCG 1412

LOCUS       AF030060                2089 bp    DNA     linear   INV 13-NOV-1997
DEFINITION  Babesia bovis strain Ur rhoptry associated protein-1 (rap-1) gene,
            complete cds.
ACCESSION   AF030060
VERSION     AF030060.1  GI:2613066
KEYWORDS    .
SOURCE      Babesia bovis.
  ORGANISM  Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2089)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2089)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164, USA
FEATURES             Location/Qualifiers
     source          1..2089
                     /organism="Babesia bovis"
                     /strain="Ur"
                     /db_xref="taxon:5865"
                     /note="isolated in Uruguay"
     gene            22..1719
                     /gene="rap-1"
                     /note="gene copy 2"
     CDS             22..1719
                     /gene="rap-1"
                     /codon_start=1
                     /product="rhoptry associated protein-1"
                     /protein_id="AAB84270.1"
                     /db_xref="GI:2613067"
                     /translation="MRIISGCVVGCLFVFSHHVSAFRHNQRVGSLAPAEVVGDLTSTL
                     ETADTLMTLRDHMHIINITKDMKHVLSNGREQIVNDVCSNAPEDSNCREVVNNYADRCEM
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                     NHGDYHYFVTGLLNNNVHEEGTDVEYLVNKVLYMATHMNYKTYLTIVNSMNAKFENRF
                     SFTKIFSRRIKQTLSDIIRWNVPEDFEERSIERITLQLFSSGYIFMLTQIPTLSKFAR
                     RYADMVKRVLLGSLTSYVEAPWYRKWIKKFRDFFSKNVTQPTKKFIEDTNEVTKNYLK
                     ANVAEPTKPKFMQDFHEKTKGYLKENVAEPTKTFEKEAPQVTKHEFDDNIGQPTKEFFR
                     EAPQQATKHFLDENIGQPTKEFFRRAPQQATKHFLDENIAQPTKEFEKDVPQVTKVITE
                     NIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKNFISAAHEGTKQFLNET
                     VGQPTKEFLNGALETTKDALHHLGKSSEERANPYDATENTTQANDSTTSNGEDTAGYL"
BASE COUNT      659 a    447 c    411 g    572 t
ORIGIN
```

```
Db    172 ATGACTCTCCGTGACCACACATGCACACATTACTTAAGGATTATATGAAAACACATGTTTGAGCAAT 231
          ||||||||||||||||||||||||||||||||||||||||                    |||
Qy     41 ValSerAspAsnPheAlaLaGlyAlaArgIleCysSerGlnValProLysGlySerAsnCysSer 60

Db    232 GGTCGGTGAGCAGATTGTAAATGATGTTTGCCTCAAATGCTCCAATGCTCCGAGGACTCCAACTGTCGT 291
          :::          ||||||||            |||:::                  ||||||||||||
Qy     61 AlaSerValSerAlaLaTyrMetSerArgCysAlaLysGlnAsnProLeuThrLeuGluSer 80

Db    292 GAGGTAGTTAACAATTATGCTGACCGTTGTGAAAATGTAGCGGATGCTTTTGACGATAAT 351
          ::::||||||||||||||||||||||||||||||||||||||            :::
Qy     81 LeuLysTyrProLeuGluLeuAlaLysTyrGlnProLeuThrLeuProLysProyGlnLeu 100

Db    352 GTCAAAATACCGTTGTATCAAGAGTACCAAACCTCTATCCTCTCAAACCCTTACCAGTTG 411
          |||||||||||||||||||||||||::::        :::              ||||||
Qy    101 GlyLeuAlaLaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGlyLys 120

Db    412 GATGCGTGCGTTCAGATTGTTCAGATTGTGCAAAGAGTGCATCGAAACGTCCGCCAGAGCAGGTAAAA 471
          |||||||||||||||||||||||::::        |||              ||||||||
Qy    121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140

Db    472 CGCGGAATGGTTGGCGTTTCAGAAAATGGACGGAGCGGAACCATGGTAGTTACCACTACTTCGTCACT 531
          |||||||||||||||||||||||||::::||::||::||:||::||||||||::::|||
Qy    141 AsnLeuLeuGluLysGlyAsnValThrArgAspAlaAsnAlaThrAspIleGluAsnPheAla 160

Db    532 GGTCTGTTGAACAACACAAATGTTGTGCACGAGGAAGGAACTACCGATGTTGAATATCTGTC 591
          |||||||                                                ||||||
Qy    161 SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrArgAsnValAspGluPhe 180

Db    592 AACAAAGGTAACTCTATAGGGCCACCATGAACTACAAGACTTATTTGACAGTAAACAGTATG 651
          :::              |||::::        ||||||||::::              |||
Qy    181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyIleLysTrpGlyIleLysLys 200

Db    652 AACGCCAAGGTTCTTCAACAAGGATTCAGCTTCACTCAACAAAAATATTCAGTGTGGTATTAAG 711
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    201 ArgGlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuGlyThrArgGluHisSer 220

Db    712 CAAACATTGAGTGATATCATCAGGTGGAATGTTCCTGAAGATTT---GAAGAAAAGGAGC 768
          |||                                    |||              |||
Qy    221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrArgThrGlnIlePro 240

Db    769 ATCGAAACGGTTATCACTCAACTTACTACAGAGCAGCTTTTTTCATCTGGTTACATTTTGC 828
          |||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValAlaGlnArgLeuLeuAlaThr 260

Db    829 ACTCTTTCAAGTTTGCAGTTCTTTATGCTGACAGGTGGTGAAGGTCTGCTGGTAGG 888
          |||||||||||||||||||||||||||||||||::::||||||||||||||||||
Qy    261 ValAlaGlyLeuTyrValAspThrProTrpTyrLysTrpIleValLysAsnPhe 280

Db    889 TTGACCTCGTACGTTGAAGCTCCTTGGTACAAAGAATGGATAAAGAAATTCAGAGACTTT 948
          |||||||||||||||||||||||||||||||::::||||::||||||||||
Qy    281 MetValAsnArgValPheIleProThrLysLysPhe------------------ 292

Db    949 TTCTCTAAAAACGTTACCCAACCTACAAAGAAGTTCATCGAGGATACTAACGAAGTTACC 1008
          ||||||                                        |||
Qy    292 ------------------------------------------------------ 292

Db   1009 AAAAACTATCTGAAAGCCAATGTTGCTGAGCCCACTAAAAAGTTTATGCAGGACACTCAC 1068
          ||||||                                                |||
Qy    292 ------------------------------------------------------ 292

Db   1069 GAAAAAAACCAAAGGCTATCTGAAAGAGAATGTAGCCGAAACCTACTAAGACTTTTTTGAAG 1128
          |||||||||||||||                              |||::::||||::
Qy    293 ------------------PheAsnLysGluIleArgGluProSerLysAlaLeuLysGlu 306

Db   1129 GAGGCTCCTCCAAGTCACCAAAAACAACTACTTCGATGATAACATTGGCACAACCTAAGG 1188
          ::::||||||||||||||||||||||||||||||
Qy    307 LysValSerThrAspThrLysAspPheGluAsnLysIleGlyLysGlyThrValAsp 326

Db   1189 TTTTTTCAGGGAAGCTCCCCAACGCCACTAAACATTTCCTAGACGAAAAACATCGGTCAACCA 1248
          |||||||||||||::::::              |||::::        |||
Qy    327 PhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGlu 346

Db   1249 ACCAAGAGAGTTCTTC---AGGGAGGCTCCTCCAAGCCCACTAAGACACTTCCTAGACGAGAAT 1305
          ||||:::              |||              |||              ||||||
Qy    347 AlaLysAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIleAsnAsnGlu 366
```

```
US-09-807-459-2 (1-458) x AF030060 (1-2089)

Alignment Scores:
Pred. No.:
Score:                              3.59e-58
Percent Similarity:                 831.50
Best Local Similarity:              51.70%
Query Match:                        35.73%

                     Length:        2089
                     Matches:       179
                     Conservative:  80
                     Mismatches:    193
                     Indels:        49
                     Gaps:          6

Qy      1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer 20
          ::::|||||||::::||||||||||||          |||||||||
Db     20 ValAspSerAlaAlaAsnAlaAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerArgAla 40
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RESULT 5
AF030058

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LOCUS       AF030058                2306 bp    DNA     linear   INV 13-NOV-1997
DEFINITION  Babesia bovis strain CG-P rhoptry associated protein-1 (rap-1)
            gene, complete cds.
ACCESSION   AF030058
VERSION     AF030058.1  GI:2613062
KEYWORDS    .
SOURCE      Babesia bovis.
  ORGANISM  Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2306)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2306)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164, USA
FEATURES             Location/Qualifiers
     source          1..2306
                     /organism="Babesia bovis"
                     /strain="CG-P"
                     /db_xref="taxon:5865"
                     /note="isolated in Campo Grande, Brazil"
     gene            22..1719
                     /gene="rap-1"
                     /note="gene copy 1"
     CDS             22..1719
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                     /codon_start=1
                     /product="rhoptry associated protein-1"
                     /protein_id="AAB84268.1"
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                     /translation="MRIISGVVGCLFLFSHHVSAFRHNQRVGSLAPAEVVGDLTSTL
                     ETADTLMTLRDHMHNITKDMKHVLSNGREQIVNDVCSNAPEDSNCREVVNNYADRCEM
                     YGCFIDNVKYPLYQEYQPLSLPNPYQLDAAFRLFKESASNPAKNSVKREWLRFRNGA
                     NHGDYHVFVTGLLNNNVVHEEGTDVEYLVNNKVLYMATMNYKFYLTVNSMNAKFFNRF
                     SFTTKIFSRRIKDTLSDIIRWNVPEDFEERSIERITQLITSSYEDYLMIQIPLSKFAR
                     RYADMVKVLLCGSLTSVVEAPMYKRWIKKFRDFFSKNVTQPTKFEIEDTNEVTKNYLK
                     ANVAEPFKKFMQDTHEKTKGYLKENVAEPTKFFFKEAPQVTKHFEDDNIGQPTKEFFR
                     EAPQATKHFLDENIGQPTKEFFREAPQATKHFLDENIGAKNFISAAHEGTKQFLNET
                     NIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKNFISAAHEGTKQFLNET
                     VGQPTKEFLNGALETTKDALHHLGKSSEEANPYDATENTTQANDSTTSNGEDTAGYL"
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ORIGIN

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Alignment Scores:
Pred. No.:
Score:                  4.04e-58
Percent Similarity:     51.70%        Length:        2306
Best Local Similarity:  35.73%        Matches:       179
Query Match:            35.25%        Mismatches:    193
DB:                     3             Conservative:  80
                                      Indels:        49
                                      Gaps:          6
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US-09-807-459-2 (1-458) x AF030058 (1-2306)

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Qy     1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuLeuAlaAlaSerGluSer 20
           :::       |||||      ||||::::||||     ||:::|||||      :::|||
Db   112 CTCGCACCTCCAGCTGAAGTGGTAGGTGATTTAACCTCCACATTGGAAACAGCTGAGATACTTTG 171

Qy    21 ValAspSerAlaAlaAsnAlaTyrMetIleAsnSerMetSerAspThrTyrLeuSerAla 40
           :::              |||          |||::       |||||||::        |||
Db   172 ATGACTCTCCGTGACCACATCCACAACATTACTAAGGATATGAAACATGTTTTGACCAAT 231

Qy    41 ValSerAspAsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSer 60
           |||            |||       ||::||::|||        :::
Db   232 GGTCGTGAGCAGGATTGTAAACATGTTTTGCCTCTAATGCTCTCCTGAGACTCCAAGCT 291

Qy    61 AlaSerValSerAlaThrTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGluSer 80
           ||||:::       |||       |||        |||                 ::       ::
Db   292 GAGGTAGTTAACAATTATGCTGACCGTTGTGAAAATGTACGGATGCTTTACGGATTGACAAT 351

Qy    81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu 100
           ::::|||||||      ||||||    ||||      ||::|||   |||   ||||:::|
Db   352 GTCAAATATCCGTTGTATCAAGAGTACCAACCTCTATCTCTTCCCAACCCTTACCAGTTG 411

Qy   101 GluLeuAlaAlaPheIleLeuPheLysGluSerAspAlaAlaSerProAlaAsnSerThrGluLys 120
           |||||||||||:::|||::||||||      |||      |||   ||:::|||   ||||||
Db   412 GATGCTGCGGCTTCAGATTGTTCAAGAGAGTGCATCCAACCCTGCCAAGAACAGCGTAAAA 471

Qy   121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
           |||       |||   |||||||||||    |||::|||      |||        |||
Db   472 CGCGAAGTGGTTGCGTTTCACAGAATGGGACCAACCATGGTGATTACCACTACTTCGTCACT 531

Qy   141 AsnLeuLeuGlyLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAla 160
           ||||||      ||||||      |||||||   |||::|||            |||
Db   532 GGTCGTCGTTGAACAACAATGTTCGCGACGAGAAGGAACTACCGGATGTGAATATCTGTC 591

Qy   161 SerArgTyrLeuTyrMetLeuThrLeuTyrTyrLysThrTyrThrAsnValAspGluPhe 180
           :::      ||::|||         |||||       ||::|||      |||::|||
Db   592 AACAAGGTACTCTATAATGGCCTACCAGAACTACAACAGACTPATTTGACAGTAAACAGTATG 651

Qy   181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrThrGlyIleLys 200
           ||::                    |||            |||||||:::|||       ||||
Db   652 AACGGCCAAGTTCTTCAAACAGATTCAGCTTCAACAAAGATTATTCAGTCGCTCGTCGTTATTAAG 711

Qy   201 ArgGlyAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAspPheGlyThrGluHisSer 220
           |||                      |||      |||::||||||   :::|||      |||
Db   712 CAAACATTGAGTGGATCATCAGGTGGAAATGTTCCTGAAGATTTT--GAAGAAGGAGC 768

Qy   221 ValSerArgLeuGluHisIleGlnThrSerSerTyrGluAspTyrMetAspThrGlnIleLeuPro 240
           |||      ||::|||            :::      |||||::|||||       |||::|||
Db   769 ATCGAACGTATCACTCAACTTACTACACGAGCTACGAAGATTACATPGTPGACCCAGAATTCCA 828

Qy   241 AlaLeuProLysPheAlaAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
           |||               |||   ||||::         |||:::   |||   :::
Db   829 ACTCTTTCCCAAGTTGCACGTCGTTATGCTGACAGGTGAAGAAGGTTCGTCGTCGTTATTAAG 888

Qy   261 ValAlaGlyTyrValAspThrProTrpTyrLysLysTyrMetLysLeuLysAsnPhe 280
           ::       |||      |||||||::|||||||      :::::|||:::|||
Db   889 TTGACCTCGTGACGTTGAAGTCCTTGGTACAAAAGAATGGATAAAGAAAATTCAGAGACTTT 948

Qy   281 MetValAsnArgValPheIleProThrArgLysLysPhe 292
           |||                  ||||||||||||||
Db   949 TTCTCTAAAAAACGTTACCCAACCTACAAAGAAGTTCATCGAGGATACTAACGAAGTTACC 1008

Qy   292 ------------------------------------------------------------------------------ 292
Db  1603 TTA 1605
```

```
Qy   367 IleAlaArgAspProSerLysLysValAlaLeuIleLeuArgLysValSerThrArgAlaGluAspLeuPhe 386
           |||::|||      |||   :::|||      :::                |||      :::
Db  1306 ATTGCTCAACCTACTAAAGAATTTTTCAAGGAATGTCCCTCCAAGTCACCAAGAGAGGTTATA 1365

Qy   387 GluAsnLysIleGluGlyGlyThrValAspPhe------------------------------- 397
           |||      ||||:::            ||| ----------
Db  1366 ACTGAGAACACATTCCTCAACCACTAAGGAGGTTCCTCAAGGAGGTTCCATCGTACCCATG 1425

Qy   398 ------IleAsnAsnGluIleIleAlaArgAspProSerLysLysValAlaLeuIleLeuArgLysValSerThrArgAlaGluAspLeuPhe 415
           ------       :::|||::|||      |||::|||      :::|||         |||
Db  1426 AAAGTCTTGAATGAAAACATTGCTCAACCTGCCAAGGAAATCATCACAGAGTTGGTACA 1485

Qy   416 GluLysAspAlaAspLeuPheGluAsnLysIleGlyGlyThrValAspPheIleAsnLys 435
           ::||||||         ||||||      :::|||::            |||::|||
Db  1486 GGGCCCAAGAAT---TTCATTTCCGCACCCATGAAGGTACTAAGCACAGTTCTTAAACGAA 1542

Qy   436 GluIleArgAspProSerLysLysValAlaLeuIleLeuArg---LysValSerThrArgGluAlaAspAsn 454
           |||::::|||:::   |||            |||      --- |||||         |||
Db  1543 ACTGTTGCCCAACCTACAAAGGAATTCCTGAACGGAGCTTAGAAAACTACTACTACAAAGACCGCA 1602

Qy   455 Leu 455
           |||
Db  1603 TTA 1605
```

```
LOCUS       AF030061     2323 bp    DNA    linear   INV 13-NOV-1997
DEFINITION  Babesia bovis strain Ur rhoptry associated protein-1 (rap-1) gene,
            complete cds.
ACCESSION   AF030061
VERSION     AF030061.1  GI:2613068
KEYWORDS    .
SOURCE      Babesia bovis.
  ORGANISM  Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2323)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2323)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164, USA
FEATURES             Location/Qualifiers
     source          1..2323
                     /organism="Babesia bovis"
                     /strain="Ur"
                     /db_xref="taxon:5865"
                     /note="isolated in Uruguay"
     gene            74..171
                     /gene="rap-1"
                     /note="gene copy 1"
     CDS             74..171
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                     /codon_start=1
                     /product="rhoptry associated protein-1"
                     /protein_id="AAB84271.1"
                     /db_xref="GI:2613069"
                     /translation="MRIISGVVGCLFLVFSHHVSAFRINQRVGSLAPAEVVGGDLTSTL
                     ETAPTLMTLRDHHMHNITKDMKHVLSNGREQIVNDVCSNAPEDSNCREVVNNYADRCEM
                     YGCPTIIDNVKPYLYQEYOPLSLNPYQLDAAFRLFKEEASNPAKNSVRREWLLRPNGA
                     NHGDYHYPVTGLLNNNVVHEEGTDVEYLVNKVLYMATNNYKYLTVNSMNAKFNRF
                     SFTKIFSRRIKQTLSDIIRWNVPEDFEERSIERITQLTSSSYEDYMLTQIPTLSKFAR
                     RYADMVKKVLLGSLTSYEAPWYKRWIEKFRDFESKNVTQPTKKFIEDTNEVKRNYLK
                     ANVAEPTKFMQDPHEKYLKENVAEPTKTFEEAPQVTKHFLDENIAQPTKEFEFKDVPQVTKVITE
                     EAPQATKHFLDDENIAQPTKTREFFREAPQATKHFLDENIAQPTKEFEFGFGTGAKNFISATHEGTKQFLNET
                     NIAQPTKFLFREVPHATMKVLNENIAQPAKEIIHEFGTGAKNFISATHEGTKQFLNET
                     VGQPTKEFLNGALETTKDALHHLGKSSEEANPVDATENTQANDSTTSNGEDFAGYL"
BASE COUNT      745 a    485 c    454 g    637 t    2 others
ORIGIN
```

```
Qy     1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer 20
         :::|||||||||:::::::::::|||||||:||||::::|||||||||||||||
Db   164 CTCGCTCCACCTGAAGTGGTAGGTTGAAAATGTACCGGATGCTTTACGATTGACAAT 223

Qy    21 ValAspSerAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla 40
         :::    ::: |||||||:||::||||||||::||||||||:||||||||||||
Db   224 ATGACTCTCCGTGACCACATGCACAACATTACTAAGGATATGAAACATGTTTTGAGCAAT 283

Qy    41 ValSerAspAsnPheAlaGluArgIleCysSerSerGlnvalProLysGlySerAsnCysSer 60
         ||||::::::||||||||::||||||||||||||:::||||||||||
Db   284 GGTCGTGACCAGATTGTAAATGATGTTTGCTCTAATGCTCCTGAGGACTCCAACTGTCGT 343

Qy    61 AlaSerValSerAlaTyrMetSerArgCysSerAlaLysGlnAspCysLeuThrLeuGlnSer 80
         |||:::   |||||||:||::||||||||||:::||||||||||||||||
Db   344 GAGGTAGTTAACAATTATGCTGACCGTTGTGAAAATGTACGGACGTTTACGATTGACAAT 403

Qy    81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAlaSerProTyrGlnLeu 100
         :::||||||||||||||||||||||:::||||||||||||||||||||
Db   404 GTCAAAATATCCGGTTGTACAGAGTACCAACCTCTATCTCTTCCAAAACCCTTACCAGTTG 463

Qy   101 GluAlaAlaPheIleLeuPheLysGluSerAspAlaAlaAsnProAlaLysAsnSerThrGlyLys 120
         ::: ||||||||||||||||||||:::|||||||||||||||||:::
Db   464 GATGCTGCGTTCAGATTGTCAAACGAAGAGCCCTGCCAAGAACAGCGTAAAA 523

Qy   121 ArgPheTrpMetArgPheArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
         |||:::||||||||||||||||||||||||||||:::|||
Db   524 CGCGAAATGGTTGCGTTTCAGAAAAATGGAGCCGAGAATTACCACTACTTCGTCACT 583

Qy   141 AsnLeuLeuGluLysAsnValThrArgAspAlaAsnAlaThrAspGluAsnPheAla 160
         ::::::|||||||::||||||||:::||||||||||||:::|||||||||
Db   584 GGTCGTTGAACACAATGTTGTCACGAGAAGGAACTACCGAGTTGAATATATCTTGTC 643

Qy   161 SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrValAspGluPhe 180
         :::::: |||||||||||||||||||||||||||:::
Db   644 AACAAGGTACTCTATATGGCTACCAAGAACTTATTCGACACAGTAAACAGTATG 703

Qy   181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLys 200
         |||::::::||||||||||||||||||||||||||||:::|||||||
Db   704 AACGGCAAGTTCTTCAACAGATTCAGCTTCACTACAAAGATATTCAGTCGTGTATTAAG 763

Qy   201 ArgAlaLeuLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAspIleGlyThrGlnHisSer 220
         |||:::   |||||||||||||||:::|||||||:::|||
Db   764 CAAACATTGAGTGAGATCATCAGATTGGAATGTTCCTGAGATTTT---GAAGAAAGAGC 820
```

```
Qy   293 ----------------PheAsnLysGluIleArgGluProSerLysSerAlaLeuLysGlu 306
                         :::   |||::::::||||||||::
Db  1009 AAAAACTATCTGAAAAGCCAAATGTTGCTGGAGCCCACTAAAAAGTTATGCAGAACATCAC 1068

Qy   307 LysValSerThrAspThrLysAspLeuPheGluGluAsnGlyIleGlyGlyThrValAsp 326
         ||||||    :::||||||||||||||||::::::|||||||||||:::
Db  1069 GAAAAAACCAAAAGGCTATCTGAAAGAGAATGTAGCCGAAACCTTACTAGACTTTTTCAAG 1128

Qy   327 PhePheAsnLysGluIleArgAspProSerLysLysLysValSerAsnAsp 346
         ||||||:::|||||||||||||||||:::
Db  1129 GAGGCTCCTCAAGTCACCAAACACTTCTTCGATGATAACATTGGCCACCACCAAGGAG 1188

Qy   347 AlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGlu 366
         ||||::::::|||||||::||||||||||:::||||||||||
Db  1189 TTTTTCAGGGAAGCTCCCCAACGCCACTAAAACATTTCCTAGACGAAAAACATCGGTCAACCA 1248

Qy   367 IleArgAspProSerLysSerAlaLeuIleLeuArgLysValSerThrGlyAlaGluAspLeuPhe 386
         |||:::||||||||||||||:::||||||||||||||:::
Db  1249 ACCAAGGAGTTCTTC---AGGGAGGCTCCTCAAGCCACTAAGCACTTCCTAGACGCAGAAT 1305

Qy   398 ----IleAsnAsnGluIleLeuArgAspProSerLysLysAlaLeuLeuLeuArg---- 415
                 |||:::||||||||||||||||||||||||||||||:::
Db  1366 ACTGAGAACATTGCTCACCAACCTACAAGGAGTTCCTAGGGAGGTTCCTCATGCTACCATG 1425

Qy   416 GluAlaAspAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPhe--------- 435
         |||:::   ||||||||||||||||||||||||||:::
Db  1486 GGCGCCAAGAAT---TTCATTTCCGGAGCCCCATGAGAGGTACTACAAGAGTTCTTAACGAA 1542

Qy   436 GluIleArgAspProSerLysSerAlaLaLeuIleArg---LysValSerThrGluAlaAspAsn 454
         |||::: ||||||::||||||||||||||||||:::|||
Db  1543 ACTGGTTGGCCAACCTACAAAGGAAATTTCTGAACGGACGCTTTGAGAACACTAAAGAGCCA 1602

Qy   455 Leu 455
         |||
Db  1603 TTA 1605
```

```
RESULT 7
BBO58MER
LOCUS       BBO58MER       1962 bp    DNA     linear   INV 28-APR-1995
DEFINITION  B.bigemina merozoite surface protein (p58) gene, complete cds.
ACCESSION   M60878
VERSION     M60878.1  GI:155860
KEYWORDS    merozoite surface protein.
SOURCE      Babesia bigemina
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 1962)
  AUTHORS   Mishra,V.S., Stephens,E.B., Dame,J.B., Perryman,L.E., McGuire,T.C.
            and McElwain,T.F.
  TITLE     Immunogenicity and sequence analysis of recombinant p58: A
            neutralization sensitive, antigenically conserved Babesia bigemina
            merozoite surface protein
  JOURNAL   Mol. Biochem. Parasitol. 47, 207-212 (1991)
  MEDLINE   92049553
FEATURES             Location/Qualifiers
     source          1..1962
                     /organism="Babesia bigemina"
                     /db_xref="taxon:5865"
                     /dev_stage="merozoite"
     gene            186..1628
                     /gene="p58"
     CDS             186..1628
                     /gene="p58"
                     /codon_start=1
                     /product="merozoite surface protein"
                     /protein_id="AAA65583.1"
                     /db_xref="GI:155861"
                     /translation="MRSFLGVCFGALLLVARSGSAIRYTHRSGVWSAEVVGGDVSKLL
                     EANEVVNAEMEATQVANKDMQSQLSNVKETIVGEVCKVAGNSTCCESVIAVVNRCDEG
                     DCLTLDSMKYKPLSLPNPYQLDDAAFMLFRESDSNPAKNEVKRFWMRSSSHGDYHIFV
                     VSLLKKNVVRDPESNDVFNFASQYFYMTTYLKYKTYLDVLDSTAAKFFNKLLAFTTRLFGF
                     GIQKALKRLVRSNLPVDLGTHPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKT
                     LLVTVSDYVIHLPAYKRWYRKRKEFIVNFFTDPAKLIMKHVSQPVKFAYTKLVPEEHRQ
                     AIRNVVGQSTHIANGVRDLSRMIKEPSQQIIREKLPHYLSKAKGAVEHVVKKVSVV
                     PIKQKDPEAAAVEETVPSDSDAETFEFEVPEEQYDAVTTQEVNSEKEVDADDAGNAE
                     TQQLPDAENEVRADDPKNEDSSSSSSDSDA"
BASE COUNT      506 a    442 c    492 g    522 t
ORIGIN

US-09-807-459-2 (1-458) x BBO58MER (1-1962)

Alignment Scores:
Pred. No.:                  7e-58
Score:                     827.50            Length:        1962
Percent Similarity:         59.12%           Matches:        181
Best Local Similarity:      41.80%           Conservative:    75
Query Match:                35.08%           Mismatches:     140
DB:                             3            Indels:          37
                                             Gaps:            12
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```
Qy    4  SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
            :::|||    :|||::|||::||||||::|||||||||||::|||||||::|||
Db  282  GCAGAGGTGGTTGGAGATGTGCCAAGACCTTGCTGGAAGCCAATGAGGTTGTCAATGCT 341

Qy   24  AlaAlaAsnAlaThrTyrMetIleAsnSerAsnSerAspTyrLeuSerAlaValSerAsp 43
            ||    :|||    ::|||    |||||    ||||::|||||    ::|||||
Db  342  GAAATGGAAGCAACTCAGGTCAACAAAGATATGCAAAAGTCAATTGTCTAAATGTTAAGGAG 401

Qy   44  AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
            :::|||||    ||||::|||    :|||    |||||||::|||:::|||||
Db  402  ACCATTGTTGGTGAGGTCTGCCAGAAAAGTTGCTGGGAAACTCTACCTCGGTGAGAGCGTA 461

Qy   64  SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
            |||||||::|||    ::|||    ::|||||||    :::
Db  462  ATTGCCTATGTTAACCGTTGTGATGAGGGCGATTGTCTGACGCTTGACAGCATG----- 515

Qy   84  ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProGlyArgGlnLeuGluAlaAla 103
            :::|||::|||    ::|||||||||||::|||    ||||||
Db  516  -----AAGTACAAGCCGTTGACTCTGCCAAATCCTTACCAGTTGGACGTGCC 563

Qy  104  PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp 123
            |||::|||||||::|||||||::|||    :::||||||    |||||||
Db  564  TTCATGCTTTTCAGGGAAAGTGATTCTAACCCTGCGAAGAATGAGGTGAAGCGGCTTCTGG 623

Qy  124  MetArgPheArgArgGlyLysAsnHisSerThrTyrPheHisAspLeuValPheAsnLeuLeu 143
            |||||||    :::|||||||    |||    :::|||    |||||||
Db  624  ATGCGGTTCGAGG-----AGCAGCCACGGCGACTACCATCACTTTGTTGTTAGCTTGTTG 677

Qy  144  GluLysAsnValThrArgAspLeuAspAlaAlaThrAsp... 163
            :::||||||    :|||||||    ::|||    :::|||||
Db  678  AAGAAGAATGTTGTTAGCCGACCCTGAATCCAATGAGTTGAGAACTTCGCCATGCAGTAC 737
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```
Qy  221  ValSerArgLeuGlnHisIleThrSerSerTyrLysAspThrGlnIlePro 240
Db  821  ATCGAACGATTCAACTCAACTTACTACGCAGCTACGAAGATTACATGTTGACCCAGATTCCA 880

Qy  241  AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
Db  881  ACTCTTTTCCAAGTTTGCACGTCGTTTATGCTGACAGTGGTAGAACGTTCTCCTCGTAGC 940

Qy  261  ValAlaGlyThrValAlaSpThrProTrpTyrLysTyrMetLysTyrLeuLysAsnPhe 280
Db  941  TTGACCTCGTACGTTGAAGCTCCTTGGTACAAAAAGATGAAATTCAGAGACTTT 1000

Qy  281  MetValAsnArgValPheIleProThrLysLysAsnPhe 292
Db 1001  TTCTCTAAAAACGTTACCCAACCTACAAAAAGAAGTTCATCGAGGATACTAACGAAGTTACC 1060

Qy  292  ---------------------------------------- 292
Db 1061  AAAAAAACTATCTGAAAGCCAATGTTCCTGACCCACTAAAAAAGTTTATGCAGGACACTCAC 1120

Qy  293  --PheAsnLysGluIleArgGluProSerLysLysGlu 306
Db 1121  GAAAAAAAAACCAAAAGCTATCTGAAAGAGATGAATGTACCGGAACCTACTAAGACTTTTTTCAAG 1180

Qy  307  LysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp 326
Db 1181  GAGGCTTCCAAGTCACCAAAAACACTTCTTCGATGATAACATTGGCCAACCCACCAAGGAG 1240

Qy  327  PhePheAsnLysGluIleArgAspAspProSerLysLysAlaLeuLeuLysGluValSerAsnAsp 346
Db 1241  TTTTTTCAGGGAAGCTCCCAAGCCACTAAACATTTCCTAGACGAAAAACATCGGTCAACCA 1300

Qy  347  AlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGlu 366
Db 1301  ACCAAGGAGTTCTTC---AGGGAGCGGCTCTCAAGCCACTAAGCACTTCCTAGACGAGAAT 1357

Qy  367  IleArgAspAlaProSerLysLysAlaLeuLeuLeuLysArgLysValAlaGluAspPhe 386
Db 1358  ATTGGCTCAACCTACTAAACATTTTTTCAAGGATGTCCCTCAAGTCACCACCAAGGAGAAGGTTATA 1417

Qy  387  GluAsnLysIleGlyGlnGlyLysThrValAspPhe 397
Db 1418  ACTGAGACAATTGCTCAACCAACTAAGGAGTTCTTCATGCTTACCATG 1477

Qy  398  -----IleAsnAsnGluIleArgAspProSerLysLysAlaLeuLeuIleArgLysValAlaTyrThr 415
Db 1478  AAAGTCTTGAAATGAAAAACATTGCTCAACCTGCCAAAGGAAATCATACATCAGTTCGGTACA 1537

Qy  416  GluAlaAspSerProLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnLys 435
Db 1538  GGCGCCAAGAAT---TTCATTCGCCACCCATGGAGGTACTAAGCCAGTTCTTAAACGAA 1594

Qy  436  GluIleArgAspAspProSerLysLysAlaLeuLeuArg---LysValSerThrGluAlaAspAsn 454
Db 1595  ACTGTTGGGCCAACCTTACAAAAGGAATTCCTGAACCGGAGGCTTTGAGAAACTACTAAAAGACGCA 1654

Qy  455  Leu 455
Db 1655  TTA 1657
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RESULT 8
I12361

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LOCUS        I12361        1962 bp        DNA        linear        PAT 26-JUL-1995
DEFINITION   Sequence 1 from patent US 5422428.
ACCESSION    I12361
VERSION      I12361.1   GI:910384
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown
             Unclassified.
REFERENCE    1 (bases 1 to 1962)
AUTHORS      McGuire,T.C., McElwain,T.F., Perryman,L.E. and Davis,W.C.
TITLE        Immunization against babesiosis using purified surface antigens of
             Babesia bigemina and similar immunogens
JOURNAL      Patent: US 5422428-A 1 06-JUN-1995;
FEATURES     Location/Qualifiers
source       1..1962
             /organism="unknown"
BASE COUNT   506 a      442 c      492 g      522 t
ORIGIN
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US-09-807-459-2 (1-458) x I12361 (1-1962)

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Alignment Scores:
Pred. No.:
Score:                     7e-58
                           827.50
Percent Similarity:        59.12%          Length:        1962
Best Local Similarity:     41.80%          Matches:        181
Query Match:               35.08%          Conservative:    75
DB:                        6               Mismatches:     140
                                           Indels:          37
                                           Gaps:            12
```

```
Qy    4 SerAspSerValGlyAspValThrLeuLysThrThrLeuLeuAlaAlaAlaSerGluSerValAspSer  23
        :: ::  :::::   ||||:::|:||||||||||:::|||:||||:|:::|||
Db  282 GCAgAGGTGGTTGGAGATGGTGCCAAGAACCTTGCTGGACAAGCCAATGCT  341

Qy   24 AlaAlaAsnAlaThrTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp  43
        ||| :||::::|||||:::||:|||:::|||||:::||:|||:|
Db  342 GAAATGGAAGCAACTCAGGTCAACAAAGATATGAAAGTCAATTGTCTAATGTGTAAGGAG  401

Qy   44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAlaSerVal  63
        :::|||    :::||||||    :::||::::|||
Db  402 ACCATTGTGGTGAGGTGCTGCGAGAAGAAAGTTGCTGGAAACGTTACCTGCGGTGAGGCGTA  461

Qy   64 SerAlaThrTyrMetSerArgCysAlaLysGlyLeuThrLeuGlnSerLeuLeuLysTyr  83
        :::|||   :::|||   |||:::|||   ||||||
Db  462 ATTGCCTATGTTAACCGTGTCTGATCAGGGGGATTGTTCTACCTGGCTGACACCATG  515

Qy   84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAsnProValProGlnIleLeuGlnAlaAlaAla  103
        ||||||    ||||||:::|||
Db  516 AAGTACAAGCCGTTGACTGTCTGCCAAATCCTTACCAGTTGGACGCTGCC  563

Qy  104 PheIleLeuPheLysGluSerAspProAlaAsnSerThrGluLysGluPheTrp  123
        ||||||||||::||| :::     |||    |||
Db  564 TTCATCCTTTTCAAGGAGAGTGATCCGGCAAATAGTACCGAGAAAGAGTTTTGG  623

Qy  124 MetArgPheArgArgGlyLysAsnHisSerTyrTyrPheHisAspLeuValPheAsnLeu  143
        ::||| :::                    :::|||:::||||||
Db  624 ATGCGCTTCGAGG---AGCAGCCACGGGGACTACCACTTGTTGTAGCTTGTTG  677

Qy  144 GluLysAsnValThrArgAspAlaAspSerAlaThrAspAspIleGluAsnPheAlaSerArgTyr  163
        :::::: |||:::       ::||||||:::|||
Db  678 AAGAAGAATGTTGTACGGGACGCCGACCCTGAAATCAAATGAGTGAGAACTTCCGATCACCGAGTAC  737

Qy  164 LeuTyrMetAlaThrLeuThrTyrThrLysThrThrAsnValAspGluPheGlyAlaLeu  183
        ||||||||||||||||||||||||||||||||
Db  738 TTCTACATGACTACGTTGACTTACACAAGACTTACCGACTTGACTTACGGCGGGCTAAG  797

Qy  184 PhePheAsnLysLeuSerPheThrArgGlyLeuPheGlyThrProGlyIleLeuLysArgAlaLeu  203
        |||||||||||||||||||||||||||||||||
Db  798 TTCTTCAACAAGCTTTCTTTCACACTCGGTCTGTTCGGTATTCCAGGAAGGGCGTTG  857

Qy  204 LysGlnIleLeuArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSerArg  223
        ||||||||| :::||||||||||:::|||
Db  858 AAGCAGTTTTGGTTAGGAGCAACCTTCCGTTGGACCTTGGAAACC---CACCCTGAGGCCACC  914

Qy  224 LeuGlnHisIleThrSerSerTyrLysAspThrArgGlnIleProAlaLeuPro  243
        :::::: ||| ||||||||||||||||||:::|||
Db  915 ATCCCGCGAAATAGCTAGGAGCAACCTTCCCGTTGACCTTGGAACC---  974

Qy  244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly  263
        ||||||||||||:::|||||||||
Db  975 TCGTTCGCTGAGCGGTTCTCCAAGATGGTCGTACTAAGACTCTTGGCTACCGTTGCAGGAC  1034

Qy  264 TyrValAspThrProTrpTyrLysTyrMetLysLeuLysAsnPheMetValAsn  283
        ||||||:::|||||||||:::|||
Db 1035 TACGTCCATTTGCCCCCGTACAAGAGTGGTTACAGGAAGTTCAGGAATTCAATTGTCGAAC  1094

Qy  284 ArgValPheIleProThrLysLysPhePheAsnLysGluIleGluArgLysProSerLys  302
        |||   ||||||
Db 1095 TTCTTTACTGACCCTGCCAAGTTGATTGAAGAACACGCGTCTTCAGCCGTGTAAAGACT  1151

Qy  303 AlaLeuLysGlyLysValSerThrArgAspThrArgLeuLeuAsnLysIleGlyGln  322
        :::     |||:::|||||||||
Db 1152 GCCTACACAAAGCTGGTCCCCGAAGAGCACAGGCCGTATCAGGAGTTCAGGAAGCCTCAA  1211

Qy  323 GlyThrValAspPhePheAsnLysGlyIleLeuArgArgAspAspLysLysGluGlyLys  342
        ::|||||||||
Db 1212 AGCACCAAGCAATATTGCCAAC---GGTGTACGTGATTTGTCAAGGATGATTAAGGAG--  1265

Qy  343 ValSerAsnAspAlaLysAspLeuProHisGluGluAsnLysIle  356
        :: ||::|||::::::|||
Db 1266 ---CCTAGCCAACAAATAATTCGTGAGAACCTGCTCACCTACCTTTCTAGGCA  1316

Qy  357 GlnGlyThrValAspPheIleLeuAsnAsnGlyIleLeuArgAsp  374
        |||:::||| ||| :::|||
Db 1317 AAGGGACGCGGTTGAGCACGTTGTTAAGAGAATCCGTTGTGCCGATAAAG---  1370

Qy  375 IleArgLysTyrValSerThrGlyLeuAlaGluLeuAspProLeuPheGluAsnLysGlnGlyThr  394
        :::::: |||
Db 1371 ---CAAAAGGGCGACCAACCATCCGAAGCACGTGTAGAGGAGAAACCGTTCCGGTCTGGC---  1424

Qy  395 ValAspPheIleGluAsnGlyIleLeuArgSerAlaLeuIleLeuArgLysValThrTyr  414
        :::|||||| :::
Db 1425 ---GAATTCCGCGGGGAAACTGAATTTGAGGTCCGATAGAAACAAATACGTCGATGCCGTGTTACT  1481

Qy  415 Thr---------------------------GluAlaAspAsp  419
        :::                          :::|||
Db 1482 ACTCAGGAGGTTAACAGCGACGAGAAGGTTGATGCCGACGAT  1520
```

US-09-807-459-2 (1-458) x I12361 (1-1962)

```
Qy    4 SerAspSerValGlyAspValThrLeuLysThrThrLeuLeuAlaAlaAlaSerGluSerValAspSer  23
Db  282 GCAgAGGTGGTTGGAGATGGTGCCAAGAACCTTGCTGGACAAGCCAATGCT  341

Qy   24 AlaAlaAsnAlaThrTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp  43
Db  342 GAAATGGAAGCAACTCAGGTCAACAAAGATATGAAAGTCAATTGTCTAATGTGTAAGGAG  401

Qy   44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAlaSerVal  63
Db  402 ACCATTGTGGTGAGGTGCTGCGAGAAGAAAGTTGCTGGAAACGTTACCTGCGGTGAGGCGTA  461

Qy   64 SerAlaThrTyrMetSerArgCysAlaLysGlyLeuThrLeuGlnSerLeuLeuLysTyr  83
Db  462 ATTGCCTATGTTAACCGTGTCTGATCAGGGGGATTGTTCTACCTGGCTGACACCATG  515

Qy   84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAsnProValProGlnIleLeuGlnAlaAlaAla  103
Db  516 AAGTACAAGCCGTTGACTGTCTGCCAAATCCTTACCAGTTGGACGCTGCC  563

Qy  104 PheIleLeuPheLysGluSerAspProAlaAsnSerThrGluLysGluPheTrp  123
Db  564 TTCATCCTTTTCAAGGAGAGTGATCCGGCAAATAGTACCGAGAAAGAGTTTTGG  623

Qy  124 MetArgPheArgArgGlyLysAsnHisSerTyrTyrPheHisAspLeuValPheAsnLeu  143
Db  624 ATGCGCTTCGAGG---AGCAGCCACGGGGACTACCACTTGTTGTAGCTTGTTG  677

Qy  144 GluLysAsnValThrArgAspAlaAspSerAlaThrAspAspIleGluAsnPheAlaSerArgTyr  163
Db  678 AAGAAGAATGTTGTACGGGACGCCGACCCTGAAATCAAATGAGTGAGAACTTCCGATCACCGAGTAC  737

Qy  164 LeuTyrMetAlaThrLeuThrTyrThrLysThrThrAsnValAspGluPheGlyAlaLeu  183
Db  738 TTCTACATGACTACGTTGACTTACACAAGACTTACCGACTTGACTTACGGCGGGCTAAG  797

Qy  184 PhePheAsnLysLeuSerPheThrArgGlyLeuPheGlyThrProGlyIleLeuLysArgAlaLeu  203
Db  798 TTCTTCAACAAGCTTTCTTTCACACTCGGTCTGTTCGGTATTCCAGGAAGGGCGTTG  857

Qy  204 LysGlnIleLeuArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSerArg  223
Db  858 AAGCAGTTTTGGTTAGGAGCAACCTTCCGTTGGACCTTGGAAACC---CACCCTGAGGCCACC  914

Qy  224 LeuGlnHisIleThrSerSerTyrLysAspThrArgGlnIleProAlaLeuPro  243
Db  915 ATCCCGCGAAATAGCTAGGAGCAACCTTCCCGTTGACCTTGGAACC---  974

Qy  244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly  263
Db  975 TCGTTCGCTGAGCGGTTCTCCAAGATGGTCGTACTAAGACTCTTGGCTACCGTTGCAGGAC  1034

Qy  264 TyrValAspThrProTrpTyrLysTyrMetLysLeuLysAsnPheMetValAsn  283
Db 1035 TACGTCCATTTGCCCCCGTACAAGAGTGGTTACAGGAAGTTCAGGAATTCAATTGTCGAAC  1094

Qy  284 ArgValPheIleProThrLysLysPhePheAsnLysGluIleGluArgLysProSerLys  302
Db 1095 TTCTTTACTGACCCTGCCAAGTTGATTGAAGAACACGCGTCTTCAGCCGTGTAAAGACT  1151
```

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Db   1095 ---TTCTTTACTGACCCTGCCAAGTTGATTATGAAGCACGTCTCTCAGCCTGTAAAGACT 1151

Qy    303 AlaLeuLysGluLysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGln 322
          |||      :::   |||      :::   :::            |||   :::||||||
Db   1152 GCCTACACAAAGCTGGTCCCCGAAGAGCACAGGCAGGCTATCAGGAATGTCGTCGGTCAA 1211

Qy    323 GlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLys 342
             |||            |||      :::||||||   |||:::   :::||||||
Db   1212 AGCACCAAGCATATTGCCAAC---GGTGTACGTGATTTGTCAAGGATGATTAAGGAG--- 1265

Qy    343 ValSerAsnAspAlaLysAspLeuPheGluAsnLysIle------------------Gly 356
                      ::::::   :::         |||:::
Db   1266 ---------CCTAGCCAACAAATAATTCGTGAGAAGCTGCCTCACTACCTTTCTAAGGCA 1316

Qy    357 GlnGlyThrValAspPheIleAsnAsnGluIleArgAsp------ProSerLysAlaLeu 374
          :::|||   |||:::   :::      :::::::::         |||   |||
Db   1317 AAGGGAGCCGTTGAGCACGTTGTTAAGAAGGTTAAATCCGTTGTGCCGATAAAG------ 1370

Qy    375 IleArgLysValSerThrGlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThr 394
             :::|||            :::|||         |||      :::      |||
Db   1371 ---CAAAAGGGCGACCAACCATCCGAAGCAGCTGTAGAGGAAACCGTTCCGTCTGGC--- 1424

Qy    395 ValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyr 414
             |||            |||         |||   :::      :::      |||
Db   1425 ---GATTCCGCGGAAACTGAATTTGAGGTCCCTGAAGAACAATACGTCGATGCTGTTACT 1481

Qy    415 Thr------------------------GluAlaAspAsp 419
          |||                        :::|||||||||
Db   1482 ACTCAGGAGGTTAACAGCGAGAAGGTTGATGCCGACGAT 1520

RESULT 9
BBODNAC
LOCUS       BBODNAC                 1962 bp    DNA     linear   INV 26-APR-1993
DEFINITION  Babesia bigemina DNA sequence.
ACCESSION   M85186
VERSION     M85186.1  GI:155879
KEYWORDS    .
SOURCE      Babesia bigemina (strain Mexico) merozoite DNA.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 1962)
  AUTHORS   Mishra,V.S., McElwain,T.F., Dame,J.B. and Stephens,E.B.
  TITLE     Isolation, sequence and differential expression of the p58 gene
            family of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 53, 149-158 (1992)
  MEDLINE   92365724
FEATURES             Location/Qualifiers
     source          1..1962
                     /organism="Babesia bigemina"
                     /strain="Mexico"
                     /db_xref="taxon:5866"
                     /dev_stage="merozoite"
BASE COUNT      505 a    442 c    493 g    522 t
ORIGIN

Alignment Scores:
Pred. No.:              8.43e-58      Length:        1962
Score:                  826.50        Matches:       181
Percent Similarity:     58.89%        Conservative:  74
Best Local Similarity:  41.80%        Mismatches:    141
Query Match:            35.04%        Indels:        37
DB:                     3             Gaps:          12

US-09-807-459-2 (1-458) x BBODNAC (1-1962)

Qy      4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
          ::::::   ||||||||||||:::||||||||||||   |||:::|||   |||::::::
Db    282 GCAGAGGTGGTTGGAGATGTGTCCAAGACCTTGCTGGAAGCCAATGAGGTTGTCAATGCT 341

Qy     24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
                   |||      :::|||   ||||||         ||||||   |||   :::
Db    342 GAAATGGAAGGAACTCAGGTCAACAAAGATATGCAAAGTCAATTGTCTAATGTTAAGGAG 401
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```
Qy     44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
                         :::|||   :::|||         |||   |||      ||||||
Db    402 ACCATTGTTGGTGAGGTCTGCGAGAAAGTTGCTGGAAACTCTACCTGCGGTGAGAGCGTA 461

Qy     64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
             ||||||::::::||||||   :::   |||||||||||||||   |||:::
Db    462 ATTGCCTATGTTAACCGTTGTGATGAGGGCGATTGTCTGACGCTTGACAGCATG------ 515

Qy     84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla 103
                      ||||||:::||||||:::||||||:::||||||||||||:::||||||
Db    516 ------------AAGTACAAGCCGTTGAGTCTGCCAAATCCTTACCAGTTGGACGCTGCC 563

Qy    104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp 123
          |||:::||||||:::|||||||||:::|||||||||   :::      ||||||||||||
Db    564 TTCATGCTTTTCAGGGAAAGTGATTCTAACCCTGCGAAGAATGAGGTGAAGCGCTTCTGG 623

Qy    124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu 143
          ||||||   |||         :::|||      :::|||      |||   :::||||||
Db    624 ATGCGTTCGAGG------AGCAGCCACGGCGACTACCATCACTTTGTTGTTAGCTTGTTG 677

Qy    144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163
          :::|||||||||   ||||||   ::::::   |||:::|||||||||||||||:::|||
Db    678 AAGAAGAATGTTGTACGCGACCCTGAATCCAATGATGTTGAGAACTTCGCATCGCAGTAC 737

Qy    164 LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183
             ||||||   |||||||||||||||||||||      ||||||         |||
Db    738 TTCTACATGACTACGTTGTACTACAAGACTTACCTGACCGTTGACTTTACGGCGGCTAAG 797

Qy    184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLysArgAlaLeu 203
          |||||||||||||||:::|||||||||   |||||||||:::||||||::::::||||||
Db    798 TTCTTCAACAAGCTTGCTTTCACAACTCGCCTGTTCGGTTTCGGTATCCAGAAGGCGTTG 857

Qy    204 LysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSerArg 223
          |||:::::::::|||||||||||||||:::|||:::||||||   |||      :::
Db    858 AAGCGTTTGGTTAGGAGCAACCTTCCCGTTGACCTTGGAACC---CACCCTGAGGCCACC 914

Qy    224 LeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIleProAlaLeuPro 243
          ::::::   |||   |||   |||   :::||||||   ||||||:::||||||:::
Db    915 ATCCGCGAAATAGCTAGCGGCTACGGCGAGTACATGATGACCCAGGTGCCTGCGATGACC 974

Qy    244 LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly 263
             ||||||:::|||||||||   |||      :::   ||||||   ||||||
Db    975 TCGTTCGCTGAGCGTTTCTCCAAGATGGCTACTAAGACTCTGTTGGTTACCGTCGGCGAC 1034

Qy    264 TyrValAspThrProTrpTyrLysLysTrpTyrMetLysLeuLysAsnPheMetValAsn 283
          ||||||      |||   ||||||:::||||||   |||   |||   |||:::||||||
Db   1035 TACGTCCATTTGCCCGCGTACAAGAGGTGGTACAGGAAGTTCAAGGAATTCATTGTGAAC 1094

Qy    284 ArgValPheIleProThrLysLysPhePheAsnLysGluIleArgGluProSerLys--- 302
                |||            |||         |||   :::   :::|||   |||
Db   1095 ---TTCTTTACTGACCCTGCCAAGTTGATTATGAAGCACGTCTCTCAGCCTGTAAAGACT 1151

Qy    303 AlaLeuLysGluLysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGln 322
          |||      :::   |||      :::   :::            |||   :::||||||
Db   1152 GCCTACACAAAGCTGGTCCCCGAAGAGCACAGGCAGGCTATCAGGAATGTCGTCGGTCAA 1211

Qy    323 GlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLys 342
             |||            |||      :::||||||   |||:::   :::||||||
Db   1212 AGCACCAAGCATATTGCCAAC---GGTGTACGTGATTTGTCAAGGATGATTAAGGAG--- 1265

Qy    343 ValSerAsnAspAlaLysAspLeuPheGluAsnLysIle------------------Gly 356
                      ::::::   :::         |||:::
Db   1266 ---------CCTAGCCAACAAATAATTCGTGAGAAGCTGCCTCACTACCTTTCTAAGGCA 1316

Qy    357 GlnGlyThrValAspPheIleAsnAsnGluIleArgAsp------ProSerLysAlaLeu 374
          :::|||   |||:::   :::      :::::::::         |||   |||
Db   1317 AAGGGAGCCGTTGAGCACGTTGTTAAGAAGGTTAAATCCGTTGTGCCGATAAAG------ 1370

Qy    375 IleArgLysValSerThrGlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThr 394
             :::|||            :::|||         |||      :::      |||
Db   1371 ---CAAAAGGGCGACCAACCATCCGAAGCAGCTGTAGAGGAAACCGTTCCGTCTGGC--- 1424
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RESULT 10
BBOMER60
BBOMER60

LOCUS       BBOMER60                1990 bp    mRNA        linear   INV 06-MAR-1995
DEFINITION  Babesia bovis 60 kDa merozoite surface protein mRNA, complete cds.
ACCESSION   M38218
VERSION     M38218.1  GI:155883
KEYWORDS    merozoite surface protein Bv60.
SOURCE      B.bovis (strain Mo7) blood stage, cDNA to mRNA, clone pBv60.
  ORGANISM  Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 1990)
  AUTHORS   Suarez,C.E., Palmer,G.H., Jasmer,D.P., Hines,S.A., Perryman,L.E.
            and McElwain,T.F.
  TITLE     Characterization of the gene encoding a 60-kilodalton Babesia bovis
            merozoite protein with conserved and surface exposed epitopes
  JOURNAL   Mol. Biochem. Parasitol. 46 (1), 45-52 (1991)
  MEDLINE   91304520
COMMENT     Draft entry and computer-readable sequence for [unpublished (1990)]
            kindly submitted
            by T.F.McElwain, 30-AUG-1990.
            Washington State University
            Dept of Veterinary Microbiology and Pathology
            Pullman, WA 99164-7040 USA.
FEATURES             Location/Qualifiers
     source          1..1990
                     /organism="Babesia bovis"
                     /strain="Mo7"
                     /db_xref="taxon:5865"
                     /clone="pBv60"
                     /tissue_type="lambda-zap II lambda-gt11"
                     /dev_stage="blood stage"
     gene            1..1990
                     /gene="Bv60"
     CDS             122..1819
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                     /codon_start=1
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                     /protein_id="AAA62695.1"
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                     /translation="MRIISGVVGCLFLVFSHVSARRHNQRVGSLAPAEVVGDLTSTL
                     ETADTLMTLRDHMHNITKDMKHVLSNGREQIVNDVCSNAPEDSNCREVVNNYADRCEM
                     YGCFTIDNVKYPLYQEYQPLSLPNYQLDAAFRLFKESASNPAKNSVAREWLRFRNGA
                     NHGDYHYFVTGLLNNNVVHEEGTTDVEYLVNRKVLYMATMNYKTLYTVNSMNAKFPNR
                     SFTTKIFSRRIRQTLSDIIRNWVPEDFEERSIERIIQLTSSYEDYMLTQIPLSKFAR
                     RYADMVKKVLLGSLTSTVEAPAMYKRWIKKFRDFSKNVTQPTFKKFIEDTNEVTKNYLK
                     ANVAEPTKKFMQDTHKTKGYLLKENVAEPTKFKFFKEAPQVTKHFFDENIGQPTKEFFR
                     EAPQAATKHFLDENIGQPTKEFFREAPQATKHFLGENIAQPTKEFFKDVPQVTKKVITE
                     NIAQPTKEFRREVPHATMKVLNENIAQPAKEIIHEFGTGAKNFISAAHEGTKQFLNET
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BASE COUNT      628 a    437 c    398 g    527 t
ORIGIN
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Alignment Scores:
Pred. No.:
Score: 826.50
Percent Similarity: 51.30%
Percent Identity: 35.53%
Best Local Similarity: 35.04%
Query Match: 3
DB:

Length: 1990
Matches: 178
Conservative: 79
Mismatches: 195
Indels: 49
Gaps: 6

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Qy    395 ValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleLeuArgLysValTyr 414
              |||                                |||
Db   1425 ---GATTCCGCGGCAAACTGAATTTGAGGTCCCTGAAGAACAATACGTCGATGCTGTTACT 1481

Qy    415 Thr----------GluAlaAspAsp 419
                       |||||||
Db   1482 ACTCAGGAGGTTAACAGCCGAGAAGGTTGATCCGACGAT 1520

Db    212 CTCGCTCCAGCTGAAGTGGTGTAGGTGGTGATGTTAACCTCCACATTGGAAACAGCTGATACTTTG 271

Qy     21 ValAspSerAlaAlaAlaAsnAlaThrTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla 40
Db    392 GAGGTAGTTAACAATTATGCTGACACGGTTGTGAAAATGTACGGATGCTTTACGATTGACAAT 451

Qy     41 ValSerAspAsnPheAlaGluArgIleCysSerSerGlnValProLysGlySerAsnSer 60
Db    272 ATGACTCTCCGTGACCACATGCACAACATTACTAAGGATATGAAACATGTTTTGAGCAAT 331

Qy     61 AlaSerValSerAlaThrTyrMetSerArgCysValAlaLysGlnAspCysLeuThrLeuSer 80
Db    332 GGTCGTCGAGCAGATGTGTAAATGATGTTTGCTCTAAGCTCCTGAGGACTCCAAACTCTCGT 391

Qy     81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAsnProTyrGlnLeu 100
Db    452 GTCAAATATCCGTTGTATCAAGAGTACCAACCTCTATCCTTCCAAACCCTTACCAGTTG 511

Qy    101 GluAlaAlaPheIleLeuPheLysGluSerAspAlaAlaAsnProAlaAsnSerThrGlyLys 120
Db    512 GATGCTGCGTTCATAGATTGTTCAAAAGAGTCGCATCGAAGAGCCCTGCCAAGAACAGGT 571

Qy    121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisSerAspLeuValPhe 140
Db    572 CGCGAAATGGTTGCGTTTCAGAAATGGACCGAACCCATGGTTGATTACCACTTCGTTCACT 631

Qy    141 AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGluIleAsnPheAla 160
Db    632 GGTCGTGTTGAACAAATGTGTCGACGAAGGAACTACCGGATGTGAATATATCTTTGTC 691

Qy    161 SerArgThrTyrLeuTyrMetAlaThrLeuThrThrTyrThrArgAsnValAspGluPhe 180
Db    692 AACAAGGTACTCTATATGGCTACCAACTACAAGACTTATTTGACAGTAAACAGTATG 751

Qy    181 GlyIleAlaSerPheAsnLysLeuSerPheThrThrThrGlyLeuPheGlyTyrIleLeuLys 200
Db    752 AACCGCCAAGTTCTTCAAACAGATTCAGCTTCACTACAAACAGATAATTCAGTTCGTATTAGG 811

Qy    201 ArgGlyAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuGlyThrGluHisSer 220
Db    812 CAAACAGTTGATGGATATCAAGGTGGAAAGTTCCGAGAGATTT---GAAGAAAGGAGC 868

Qy    221 ValSerArgGluLeuGlnHisIleLeuThrSerSerTyrLysAspThrTyrMetAspThrGlnIlePro 240
Db    869 ATCGAAACGTATCACTCAAACTTACTACGGAGTACCAAAAGAAGTTCATCGAGGATACTAACGGA 928

Qy    241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnIleArgLeuLeuAlaThr 260
Db    929 ACTCTTTCCAAGTTTGCCACGTCGTTTATGCTCGACACTGGTGAGAGAAGGTTCTCCTCGGTAGC 988

Qy    261 ValAlaLeuGlyTyrValAlaAspThrProThrProTyrLysLysTrpTyrMetLysLeuLysAsnPhe 280
Db    989 TTGACCTCGTACGTTGAAGCTCCTTGGTACAAAAGATGGATAAAAAGAAATTCAGAGACTTT 1048

Qy    281 MetValAsnArgValPheIleGluProThrLysLysPhe------------------ 292
Db   1049 TTCTCTAAAAACGTTACCCAACCTACAAAAGAAGTTCATCGAGGATACTAACGAAGTTACC 1108

Qy    292 --------------------------------- 292
Db   1109 AAAAAACTATCTGAAAGCCCAATGTTCTGAGCCCACTAAAAAGTTTATGCAGGAGCACTCAC 1168

Qy    293 -------------PheAsnLysGluIleArgAspProSerLysAlaLeuIleLeuGlu 306
Db   1169 GAAAAAACCAAAGGCTATCTGAAAGAATTGGCGAAGCTAGACGCTAAAACACATTTTTTCAAG 1228

Qy    307 LysValSerThrAspThrLysThrLeuAsnLysIleGlyGlnGlyThrValAsp 326
Db   1229 GAGGCTTCCTCAAGTCAACAAAACACTTCTTCGATGAGAACAATTGGCAACCCAACCACAGGAG 1288

Qy    327 PhePheAsnLysGluIleArgAspProSerLysAlaLeuIleLeuGluLysValSerAsnAsp 346
Db   1289 TTTTTCAGGAAGCTCCCCAAGGCCACTAAAACACATTTCCTAGACGAAAAAACATCGGTCAACCA 1348
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US-09-807-459-2 (1-458) x BBOMER60 (1-1990)

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Qy      1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaLeuAlaSerGluSer 20
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8.58e-58

LOCUS   AF030057   2087 bp   DNA   linear   INV 13-NOV-1997
DEFINITION Babesia bovis strain CG-P rhoptry associated protein-1 (rap-1)
            gene, complete cds.
ACCESSION   AF030057
VERSION   AF030057.1 GI:2613060
KEYWORDS   .
SOURCE   Babesia bovis.
  ORGANISM Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 2087)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE   Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 2087)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164, USA
FEATURES   Location/Qualifiers
     source   1..2087
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                     /strain="CG-P"
                     /db_xref="taxon:5865"
                     /note="isolated in Campo Grande, Brazil"
     gene   22..1719
                     /gene="rap-1"
                     /note="gene copy 2"
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                     /translation="MRIISGVVGCLFLVPSHHVSAFRINQRVGSLAPAEVVGDLTSTL
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                     NHGDYHYFVTGLLNNNVHEEGTDVEIKLVNKYLVMATWNYKTYLTVNSMNAKEFNRE
                     SFTTKIFSRRIKQTLSDIIRWNVPEDFEERSIERITQLTRSSYEDYMLTQIPTLSKFAR
                     RVADMVKVLLGSLTSVYEAPWYKRWIKFKRDFFSKNVTQPTKHFEIEDTNEVTKNYLK
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RESULT 11

US-09-807-459-2 (1-458) x AF030057 (1-2087)

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Alignment Scores:
Pred. No.:
Score: 9.09e-58
                        826.50
Percent Similarity: 51.50%
Best Local Similarity: 35.53%
Query Match: 35.04%

Length: 2087
Matches: 178
Conservative: 80
Mismatches: 194
Indels: 49
Gaps: 6

BASE COUNT   670 a   449 c   410 g   558 t
ORIGIN

Qy   347 AlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGlu 366
          |||::: ||| ||| |||:::||||
Db   1349 AccAAggAgttcttC---AgggAggcctcctCaagCcaCtaCacttcttAggCgAgAAt 1405

Qy   367 IleArgAspProSerLysAlaLeuIleArgLysValSerThrGlyAlaGluAspLeuPhe 386
          |||:::||| |||:::
Db   1406 ATTGCTCAACCTACTAAAGGAGAATTTTTCAAGGATGTGCCCTCAAGTCACCAAGAAGGT TATA 1465

Qy   387 GluAsnLysIleGlyGlnGlyThrValAspPhe------ 397
          ||| ||| ||| :::||
Db   1466 ACTGAGAACAATTGCTCAACCAACTAAAGGAGAGTTCCTGAGGG------- 1525

Qy   398 ------IleAsnAsnGluIleLeuArgAspProSerLysAlaLeuIleArgLysValTyrThr 415
          :::||| ||||| |||:::||| |||
Db   1526 AAAGTCTTGAATGAAAACATTGCTCAACCTGCCAAGGAAAATCATCAGACAGTTTCGGTACA 1585

Qy   416 GluAlaAspAlaSerLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnLys 435
          ||| ::: ||| ||| |||
Db   1586 GGCGCCAAGAAT---TTCATTCGCCAGCCCATGAAGGTACTAACGCAGTTGTTAAACGAA 1642

Qy   436 GluIleLeuArgAspProSerLysAlaLeuIleArg---LysValSerThrGluAlaAspAsn 454
          |||::: |||:::|||
Db   1643 ACTGTTGGGCCACCTACAAAGGAATTCCTGAACGGAGCTTTAGAAACTACTAAAGACGCA 1702

Qy   455 Leu 455
          |||
Db   1703 TTA 1705

Qy   1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer 20
          |||||||||:::||||||||||||||||||||:::||||||||||||:::||||
Db   1 CTCGCTCCAGCCtgaAAGTCGtAGGTGATTTAACCTCCACATTGGaAAACAGCTACTTTG 100

Qy   21 ValAlaSpSerAlaAlaLysAlaTyrMetIleAsnSerAsnAspMetSerAspTyrLeuSerAla 40
          |||:::||||||||||||||||:::|||||||||||||||
Db   112 GTCAAAATAATCCGTTGTATCAAcgAGTACCAACCTCTATCTTCAAACCCTTACCAGTTG 171

Qy   41 ValSerAspAsnPheAlaGluArgIleCysSerGlnIleLeuCysSerGlnAsnCysSer 60
          ||| :::|||||||||
Db   172 ATGACTCTCCGTGACCACATGCACAACATTACTAAGGATATGAAACAtGTTTTGAGCAAT 231

Qy   61 AlaSerValSerArgArgCysAlaLysGlyAspCysLeuThrLeuGlnSer 80
          |||:::||||||
Db   232 GGTCGTGGAGCAGGATTGTAAAATGAtTGTTTGGCTCTTAATGCTCCGAGGACTCCAACTGTCGT 291

Qy   81 LeuLysTyrProLeuGlnAlaLysTyrGlnProLeuThrLeuProAlaProTyrGlnLeu 100
          :::||||||||||||||||:::|||
Db   292 GAGGTAGTTAACAAAtTAATGCTCAACCgTTGtGAAATGGACCGGTTACGGATTGCACAAT 351

Qy   101 GluAlaAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys 120
          :::||||||||||||
Db   352 GTCAAAATAATCCGTTGTATCAAcgAGTACCAACCTCTATCTTCAAACCCTTACCAGTTG 411

Qy   121 AsnLeuLeuGluLysAsnLysValThrArgArgAspAlaAspAlaThrAspIleGluAsnPheAla 140
          |||:::||||||
Db   412 GATGCTGCCGGTTCAGATTGTTCAGAAAGAGTGCATCGAACCCTGCCAAGAACAGCGTAAA 471

Qy   141 AsnLeuLeuGluLysAsnValThrArgArgAspAlaAspAlaThrAspIleGluAsnPheAla 160
          |||:::
Db   472 CCCGGAATGGTTCGCGTTTCAGAAAGAGGACCGGAACCACATGGTGATTACCACTACTTCGTCACT 531

Qy   161 SerArgTyrLeuTyrMetAlaThrTrpTyrTyrLysThrTyrThrArgAsnValAspGluPhe 180
          |||:::
Db   532 GGTCCTGTTGAACAACATGTTGTGCACGGAGGAAGACTACCCGATTGTGAAATATCTTGTC 591

Qy   181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyThrGlyIleLys 200
          :::||||||||||
Db   592 AACAAGGTACTCTTATATGGGCTACCaTGAACTACATCAAGACTTATTTGACAGTAAACAGTATG 651

Qy   201 ArgAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAspIleGlyThrGluHisSer 220
          |||:::
Db   652 AACGGCCAAGTTCTTCAACAGATATTCAGTGAAGAATATAATGCTCAGTTGATTAACTTTAAG 711

Qy   221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro 240
          |||:::|||||||||
Db   712 CAAACATTGAGTGATATCATCAGGTGGAATGTTCCTGAAGATTT-----GAAGAAAGGAGC 768

Qy   241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
          |||:::|||||||||
Db   769 ATCGAACGTATCACTCAACTTACTAGGCAGCAACAAGTACATTTGACCCAGATTCCA 828

Qy   261 ValAlaGlyTyrValAspThrProThrPTyrLysLysTyrTyrMetLysLysAspAsnPhe 280
          |||:::|||||||
Db   829 ACTCTTTCCAAGTTTGCACGTCGTTAtGCTGACATGGTGAAGGTTTTGCTCGGTAGC 888

Qy   281 MetValAsnArgValPheIleProThrThrLysLysPhe---------------- 292
          :::|||
Db   889 TTGACCTCGTACGTTGAAGCTCCTTGGTACAAAAGATGGATAAAAGAAAATTCAGAGACTTT 948

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RESULT 12
AF030053
AF030053

LOCUS       AF030053       2089 bp    DNA      linear   INV 13-NOV-1997
DEFINITION  Babesia bovis strain S2p rhoptry associated protein-1 (rap-1) gene,
            complete cds.
ACCESSION   AF030053
VERSION     AF030053.1  GI:2613052
KEYWORDS    
SOURCE      Babesia bovis.
ORGANISM    Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 2089)
AUTHORS     Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE       Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 2089)
AUTHORS     Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
TITLE       Direct Submission
JOURNAL     Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164, USA
FEATURES             Location/Qualifiers
     source          1..2089
                     /organism="Babesia bovis"
                     /strain="S2p"
                     /db_xref="taxon:5865"
     gene            22..1721
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                     /note="gene copy 2"
     CDS             22..1719
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                     SFTTKIFSRRIRQTLSDIIRWNPEDEEFERSIERITQLTSSYEDYMLTQIPTLSKFAR
                     RYADMVKKVLLGSSLTSYVEAPWYKMRWIKKFRDFFSKNVTQPTKFKFFIEDTNEVTKNYLK
                     ANVAEPPTKKFMQDTHEKRKGYLEKENVAEPTKHFKIPFKEFKDVPQVTKKVITE
                     EAPQATKHFLDENIGQPFKEFFREAPQATKHFLGENIAQPTKEFF
                     NIAQPTKEFLREVPHAFMKVLNENIAQPAKEIIHEFGTGAKNFISAHEGTGQFLNET
                     VGQPTKEFLNGALETTKDALLHHLGKSSEEANLYDATENTTQANDSTTSNGEDTAGYL"
BASE COUNT      659 a    445 c    412 g    573 t
ORIGIN

Alignment Scores:
Pred. No.:                                        Length:              2089
Score:                           9.1e-58          Matches:              178
Percent Similarity:              826.50           Conservative:          79
Best Local Similarity:           51.30%           Mismatches:           195
Query Match:                     35.53%           Indels:                49
DB:                              35.04%           Gaps:                   6
                                   3

US-09-807-459-2 (1-458) x AF030053 (1-2089)

Qy      1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaLaSerGluSer   20
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Qy     21 ValAspSerAlaAlaAlaSerAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla   40
          :::    |||                 |||           |||
Db    352 GTCAAATATCCGTTGTATCAAGAGTACCAACCTCTATCTCTTCCAAACCCTTACCAGTTG  411

Qy     41 ValSerAspAsnPheAlaGluArgIleCysSerSerGlnValProLysGlySerAsnCysSer   60
          :::|||   |||           |||
Db    412 GATGCTGCGTTCAGATTGTTTAAAGAGACTGCATCGAACCCTGCCAAGAAACAGGGTAAA  471

Qy     61 AlaSerValSerAlaThrMetSerArgCysAlaLysGlnAspCysLeuUThrLeuGlnSer   80
          :::||:
Db    472 CGCCAAATGGTTACCTTTCGAAATGGAGCGGACCGACCATGGTGATTACCACTACTTGTCACT  531

Qy     81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAlaSerProTyrGlnLeu  100
          ::|||||||||||
Db    532 GGTCTGTTCAACAACAATGTGTGCACAGGAGGAACTACCGAATGTGAAATATCTTCTGTC  591

Qy    101 GlnAlaAlaAlaPheIleLeuPheLysSerGluSerAspAlaAsnProAlaAsnSerThrGluLys  120
          ::::|||||||
Db    592 AACAAAGGTACTCTATATGGCTACCACAAGACTTATTTTGACAGTGAAACAAGTAAAAG  651

Qy    121 ArgPheTrpPheMetArgPheArgArgGlyLysAspHisSerTyrPheHisAspLeuValPhe   140
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Db    652 AACGCCAAGTTCTTCAACAACAGATCAGATTTCAGCTTCACTCAACAAAGATAATTCAGTGCGTATTAGG  711

Qy    141 AsnLeuLeuGluLysAsnValThrArgAspAlaThrAspIleGluAsnPheAla  160
          :::|||||:::
Db    472 CGGCAAATGGTTACCTTTCGAAATGGAGCGGACCGACCATGGTGATTACCACTACT  531

Qy    161 SerArgTyrLeuTyrMetAlaThrLeuTyrArgTyrIleLysThrTyrArgAsnValAspGluPhe  180
          :::|||:::  ||||||||||||||:::
Db    592 GGTCTGTTCAACAACAATGTGTGCACAGGAGGAACTACCGAATGTGAAATATCTTCTGTC  591

Qy    181 GlyAlaSerPhePheAsnLysLeuUSerPheThrThrGlyLeuPheGlyTrpGlyIleIleLys  200
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Db    652 AACGCCAAGTTCTTCAACAACAGATCAGATTTCAGCTTCACTCAACAAAGATAATTCAGTGCGTATTAGG  711
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Db    347 ...

Db   1009 AAAAACTATCTGAAAGCCAATGTTCCTGAGCCCACTAAAAAGTTTATGCAGGACACTCAC 1068
Qy    293 -----PheAsnLysGluIleArgGluProSerLysAlaLeuLysGlu  306

Db   1069 GAAAAAAAACAAAAGGCTACTGAAAGAGAATGTAGCCGAACCTACTAAAGACTTTTTCAAG 1128
Qy    307 LysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyIleGlyThrValAsp 326

Db   1129 GAGGCTCCTCAAGTCACCAAAACACTTCTTGATGATAACACTGGCCAACCCAACCAAGGAG 1188
Qy    327 PheGluAsnLysGluIleArgAspProSerLysAlaLeuIleLysGluLysGlyValSerAsnAsp 346

Db   1189 TTTTTCAGGGAAGCTCCCCAAGCCACTAAACATTCCTAGACGAAAACATGGTCAACCA 1248
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Db   1249 ACCAAGGAGTTCTTC---AGGGAGGCGCTCTCAAGCCACTAAGCACTTCCTAGACGAGAAT 1305
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Db   1306 ATTGCTCAACCTACTAAAGAGAATTTTTCAACGGAGGTRCCCTCAAGTCACCAAGAAGGTTATA 1365
Qy    387 GluAsnLysIleGlyIleGlyThrValAspPhe---------------------------- 397

Db   1366 ACTGAGAACAATTGCTCAACCACTAAGGAGAGTTCCTTAGGGAGGTTCCTCATGCTACCATG 1425
Qy    398 ------IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyrThr 415

Db   1426 AAAGTCTTGAATGAAAAACAATTGCTCAACCTGCCAAGAAATCATACATGAGTTTGGTACA 1485
Qy    416 GluAlaAspAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIleAsnLys 435

Db   1486 GGCGGCCAAGAAT---TTCATTTCCCAGCCCATGAGGTACTAAGGCAGTTCTTAAACGAA 1542
Qy    436 GluIleArgAspProSerLysAlaLeuIleArg--LysValSerThrGluAlaAspAsn 454

Db   1543 ACTGTTGGCCAACCTACAAAGGAATTCCTGAACGGAGGCTTTAGAAACTACTAACAGCCA 1602
Qy    455 Leu 455
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Db   1603 TTA 1605
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RESULT 13
LOCUS       AF030054                2089 bp    DNA     linear   INV 13-NOV-1997
DEFINITION  Babesia bovis strain T2b rhoptry associated protein-1 (rap-1) gene,
            complete cds.
ACCESSION   AF030054
VERSION     AF030054.1  GI:2613054
KEYWORDS    .
SOURCE      Babesia bovis.
  ORGANISM  Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2089)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2089)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164, USA
FEATURES             Location/Qualifiers
     source          1..2089
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                     /strain="t2b"
                     /db_xref="taxon:5865"
                     /note="isolated in Texas, USA"
     gene            23..1722
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     CDS             23..1720
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                     NIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKNFISAAHECTKQFLNET
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BASE COUNT      657 a    444 c    414 g    574 t
ORIGIN
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US-09-807-459-2 (1-458) x AF030054 (1-2089)

Alignment Scores:
Pred. No.:          9.1e-58
Score:               826.50        Length:            2089
Percent Similarity:  51.30%        Matches:            178
Best Local Similarity: 35.53%      Conservative:        79
Query Match:         35.04%        Mismatches:         195
DB:                     3          Indels:              49
                                   Gaps:                 6
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Qy    1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaLeuAlaSerGluSer  20
        :||:||      :                        :::|||  |||
Db  113 CTCGCTCCAGCTGAGGTGGTAGGTGATTTAACCTCCACATTGAAACAGCTGATACTTTG  172

Qy   21 ValAspSerAlaAlaAsnAlaAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla  40
        :||        :::|||                |||||
Db  173 ATGACTCTCCGTGACCACATCCAACATACTAAGGATATGAAACATGTTTTGACAAT  232

Qy   41 ValSerAspAsnPheLeuGluArgLeuCysSerGlnValProLysGlySerAsnCysSer  60
        |||:|||||                     ||:|||||
Db  233 GGTCGTGAGCAGATTGTAAATGATGTTTGCTCTAATGCTCCTGAGGAACTCCAAACTGTCGT  292

Qy   61 AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer  80
        |||:::                |||            ||
Db  293 GAGGTAGTTAACAATTATGCTGACCGTTGTGAAATGTACGGATGCTTTACGATTGACAAT  352

Qy   81 LeuLysTyrProLeuGluLeuAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu  100
        :::|||||||   |||||||  :::::|||
Db  353 GTCAAATATCCGTTGTATCAAGAGTACCAACCTCTATCTCTTCCAAACCCTTACCAGTTG  412

Qy  101 GluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys  120
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Db  413 ...
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Qy   121  ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe   140
            :: ::||   |||  ||||  ||  ::||    ||||| |
Db   473  CGCGAAATGGTTGCGTTTCACAAAATGGAGGCGAAACATGGTAGACTACTTCGTCACT     532

Qy   141  AsnLeuLeuGlyLysAsnValThrArgAspAlaAspAlaThrAspIleLeuAsnPheAla   160
            ||| |||| ||:: |||||||||||||  ::||    |||||||:||:|||
Db   533  GGTCTGTTGAACACAAATGTTGTGCACGAGGAAGGAACTACCGATGTTGAATATCTTGTC   592

Qy   161  SerArgTyrTyrLeuThrTyrMetAlaThrHisLeuThrTyrTyrLysThrTyrThrAsnValAspGluPhe  180
            ||| :::|||||||||| ||| ||:::|||||||| ||| :::|||||
Db   593  AACAAGGTACTCTATATGGCTACCATGAACTACAAGACTTATTTGACAGTAAACAGTATG   652

Qy   181  GlyAlaSerPhePheAsnLysLeuSerProPheThrThrGlyLeuPheGlyTyrIleLeuLys  200
            :::||| ||||||||| |||:::|||||||||  ||:::|||||||||||
Db   653  AACGCCAAGTTCTTCAACAGATTCAGCTTCACTACAAAGATAATTCAGTCGTGTATTAGG   712

Qy   201  ArgAlaLeuLysGlnIleIleLeuLysArgSerAsnLeuProLeuAspIleGlyThrGluHisSer  220
            :::||||||:::|||||||||:||  :::|||||| |||  ::--GAAGAAAGGAGC
Db   713  CAAACATTGAGTGATATCATCAGGTGGAATGTTCCTGAAGATTTT--GAAGAAAGGAGC   769

Qy   221  ValSerArgArgLeuGlnHisIleIleThrSerSerThrTyrArgLysAspTyrMetAspThrGlnIleIlePro  240
            :::||:::|||||| :::|||||||||||||||||||||:::|||
Db   770  ATCGAACGTATCACTCAACTTACTTACCGAAGATTACAGTTGACCCAGATTCCA        829

Qy   241  AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr   260
            |||||:::|||||| |||||||||:::|||||||||| :::|||||||||||
Db   830  ACTCTTCCAAGTTTGCACGTTCGGTTATGCTGACATGGTGAAGAAGGTTCTGCTCGGTAGC  889

Qy   261  ValAlaLysGlyThrTyrValAspThrProTrpTyrLysLysTrpPheTyrMetLysValLeuLysAsnPhe  280
            :::|||||| ||| :::|||||||||||||||  ::: |||:::||
Db   890  TTGACCTCGTACGTTCCTTGGTACAAAAGATGGATAAAGAAATTCAGAGATTTT       949

Qy   281  MetValAsnArgValPheIleProThrLysSerPhe---------------------------  292
            |||  :::|||||||||||||||||||||||||||
Db   950  TTCTCTAAAAACGTTACCCAACCTACAAAGAAAGTTCATCGAGGAGTTACC          1009

Qy   292  -----------------------------------------------------------  292
            :::
Db  1010  AAAAACTATCTGAAAGCCAATGTTGCTGAGCCCACTAAAAAAGTTTATGCAGGACACTCAC 1069

Qy   293  -------------PheAsnLysGluIleArgGlnProSerLysAlaLeuLysGlu        306
                         |||  ||||:::||||||:::|||||||||||:::||
Db  1070  GAAAAAACCAAAAGGCTATCTGAACAGAAATGAGCCCACTAAGAACTTTTTTTCAAG     1129

Qy   307  LysValSerThrAspThrLysSerAspLeuPheGluAsnLysIleGlyLysGlyThrValAsp  326
            :::|||||||||||| ||||| :::||||||||| ||:::|||||||||
Db  1130  GAGGCTCCTCCAAGTCACCAAACACACTTCTTCGATGAGAACATTGGCCAACCCCACCAAGGAG 1189

Qy   327  PhePheAsnHisGlyIleArgAspProSerLysAlaLeuLysGluLysGlyValSerAsnAsp  346
            |||||| :::||| ||||||:::||||||:::|||||||||||||
Db  1190  TTTTTCAGGGAAGCTCCCCAAGCCACTAAACATTCCTAGAACGAAAACATGGTCAACCA    1249

Qy   347  AlaLysSerAspLeuPheGluAsnLysIleGlyLysGlyThrValAspPheIleAsnAsnGlu  366
            :::||||||||||| :::|||||||||||  ::: ||||||
Db  1250  ACCAAGGAGTTCTTC---AGGGAGGCTCCTCAAGCCACTTCCTAGGCGAGAAT         1306

Qy   367  IleArgAspProSerLysAlaLeuIleLeuArgGlyValSerLysThrGlyLysAlaGluAspLeuPhe  386
            ||||||:::||||||:||||||||||||||:::|||||||||||||
Db  1307  ATTGCTCACCTACTAAAGAATTTTCAAGGATGTCCCAAGTCACCAAGAAGGTTATA      1366

Qy   387  GluAsnLysIleGlyLysGlyThrValAspPhe-------------------------   397
            :::|||||||||||||||  :::||
Db  1367  ACTGGAGAACATTGCTCAACAACTAAGGACGTTCCTCATGCCACCATG            1426

Qy   398  -----IleAsnAsnGlyIleLeuArgAspProSerLysAlaLeuIleLeuArgLysValThrTyrThr  415
                  |||:::||| ||||||:::||||||:::||||||||||||:||:||||
Db  1427  AAAGTCTTGAATGAAAAACATTGCTCAACCTCCAAGAAATCATGAGTTTGGTACA       1486

Qy   416  GluAlaAspAspLeuPheGluAsnLysIleGlyLysGlyThrValAspPheIleAsnLys   435
            :: ||:||:||||||:::|||||||||||| |||:::|||||||||:::
Db  1487  GGCGCCAAGAAT--TTCATTCCCAGCCCATGAAGGTACTAAGCAGTTCTTAAACGAA     1543

Qy   436  GluIleArgAspProSerLysAlaLeuIleLeuArg---LysValSerThrGluAlaAspAsn  454
            :::        |||||:::|||            :::     |||      |||
Db  1544  ACTGTTGGCCACCTACAAAAGGAATTCCTGAACGGAGCTTTAGAAACTACTAAAGACCCA   1603

Qy   455  Leu  455
            |||
Db  1604  TTA  1606
```

RESULT 14

AF030055

```
LOCUS       AF030055                2089 bp    DNA     linear   INV 13-NOV-1997
DEFINITION  Babesia bovis strain R1A rhoptry associated protein-1 (rap-1) gene,
            complete cds.
ACCESSION   AF030055
VERSION     AF030055.1  GI:2613056
KEYWORDS    .
SOURCE      Babesia bovis.
  ORGANISM  Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2089)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2089)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164, USA
FEATURES             Location/Qualifiers
     source          1..2089
                     /organism="Babesia bovis"
                     /strain="R1A"
                     /db_xref="taxon:5865"
                     /note="isolated in Argentina"
     gene            22..1719
                     /gene="rap-1"
                     /note="gene copy 2"
     CDS             22..1719
                     /gene="rap-1"
                     /codon_start=1
                     /product="rhoptry associated protein-1"
                     /protein_id="AAB84265.1"
                     /db_xref="GI:2613057"
                     /translation="MRISGVVGCLFLVFSHHVSAFRHNQRVGSLAPAEVVGDLTSTL
                     ETADTLMTLRDHMHNITRDMKHVLSNGREQIVNDVCSNAPEDSNCREVVNNYADRCEM
                     YGCFTIDNVKYPLYQEYQPSLPNPYQLDAAFRLFKESASNPAKNSVKREWLRFRNGA
                     NHGDYHYFVTGLLNNNVHEEGTGVEVLVNKVLYMATMNYKTYLTVNSMNAKFFNRF
                     SFTTKIFSRRIRQTLSDIIRWNPEDFEERSIERITLQLTSSYEDYMLTQIPTLSKFAR
                     RYADMVKKVLLGSLTSVYEAPWYKRWIKKFRDEFSKNVTQPTKFKFIEDTNEVTKNYLK
                     ANVAEPTKFKMQDTHEKTRKGYLKENVAEPTKHFKKEAPQVTKHFDENIGQPTKEFFR
                     EAPQATKIHFLDENIGQPTKEFFREAPQATKHFLGENIAQPTKEFFKDVPQVTKRVITE
                     NIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKNFISAAHEGTKQFLNET
                     VGQPTKEFLNGALETTKDALHHLGKSSEEANLYDATENTQANDSTTSNGEDTAGYL"
ORIGIN
BASE COUNT      657 a    447 c    414 g    571 t
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Alignment Scores:

Pred. No.:	9.1e-58
Score:	826.50
Percent Similarity:	51.30%
Best Local Similarity:	35.53%
Query Match:	35.04%
DB:	

Length:	2089
Matches:	178
Conservative:	79
Mismatches:	195
Indels:	49
Gaps:	6

US-09-807-459-2 (1-458) x AF030055 (1-2089)

```
Qy     1  MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer   20
            ::||||||:||||||:::||||||||||||||||::||||||:||:||||
Db   112  CTCGCTCCAGCTGAAGTGGTAGGTGATTTAACCTCCACATTGGAAACAGCTGATACTCTG   171
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Qy   21 ValAspSerAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla   40
            |||      ::           |||
Db  172 ATGACTCTCCGTGACCACATTGCACAACATTACTCAGGAATATGAAACATGTTTGAGCAAT  231

Qy   41 ValSerAspAsnPheAlaLeuArgIleCysSerGlnValProLysGlySerAsnCysSer   60
           |||::||||| :::
Db  232 GGTGCTGAGCAGATTGTAAATGATGTTTGCTCTAATGCTCCTGAGGACTCCAACTGTCGT  291

Qy   61 AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer   80
           ||||      ::      ||
Db  292 GAGGTAGTTAACAATTATGCTGACCGTGTGTGAAATGTAGGATCCTTTACGATTGACAAT  351

Qy   81 LeuLysTyrProLeuGlnValAlaLysTyrGlnProProTyrGlnLeu             100
           :::|||||||:::
Db  352 GTCAAAAATCCGTTGTAAGCAAGAGTACCAACCTCTATCTTCCAAACCCTTACCAGTTG   411

Qy  101 GlnAlaAlaPheIleLeuPheLysGluSerAspAlaAsnSerThrGlyLys          120
           :||||||:||| ::|:::       |||
Db  412 GATGCTGCGTTCAGATTGTTCAAAGAGAGTGATGCTAACAGCTCTGGAAAA          471

Qy  121 ArgPheTrpMetArgPheArgArgGlyLysHisSerTyrPheHisAspLeuValPhe     140
           ||| |::||::||:||||||| |||
Db  472 CGCCAAATGGTTGCCTTTCAGAAATGGAGGGAACCCATGGTGATTACCACTACTTCACT   531

Qy  141 AsnLeuLeuGluLysAsnValThrArgAspAlaAlaThrArgAspIleGluAsnPheAla  160
           |||||||::::::||
Db  532 GGTTCGTGTTGAACAACAATGTTGTGTCCACGAGGAGGAACTACCGAATGTTGAAATATCTTGTC  591

Qy  161 SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPhe  180
           :::: ||
Db  592 AACAAGGTACTCTATATGGCTACACTTTACTACAAGACTTATACCAATGTTGAC       651

Qy  181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrArgThrGlyLeuGlyIleIleLys  200
           |||||||| ||:::
Db  652 AACGCCAAGTTCTTCAACAAGCTTAGCTTCACTACTAGAACAGGATTAGGTATCATTAAA  711

Qy  201 ArgAlaLeuLysGlnIleIleGluArgSerAsnLeuProLeuAspGlyThrGluHisSer  220
           ||| ||
Db  712 CAAACATTGAGTGATATCATCAGGTGGAATGTTCCTGAAGATTTT--GAAGAAAGGAGC   768

Qy  221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAlaProPheGlnIlePro  240
           :: ||| ||:
Db  769 ATCGAACGTATCACTCAACTTACATCAAGATTACAAGTTGAACAAGATTCCA         828

Qy  241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr  260
           ||||| :||
Db  829 ACTCTTTCCAAGTTTGCAAGTCGTTATCCTGACATGGTGAAGAGAGTTCTGCTCGGTAGC  888

Qy  261 ValAlaAlaGlyTyrValAspThrProTrpProTyrLysLysTrpTyrMetLeuLysAsnPhe  280
           ||||||| :::
Db  889 TTGACCTGTACGTTGAGAGCTCCTTGGTTACAAAAAGATGGATAAAAAGATTCAGAGACTTT  948

Qy  281 MetValAsnArgValPheIleProThrHisLysArgPhe--------------         292
           ||
Db  949 TTCTCTAAAAACGTTACCCAACTACAAAGAAGTTCATCGAGGATACTAACGAAGTTACC  1008

Qy  292 -------------------------------------------------------      292
Db 1009 AAAAACTATCTGAAAGCCAATGTTGCTGAGGCCACTAAAAAGTTTATGCAGGACACTCAC  1068

Qy  293 -----------PheAsnLysGluLeuArgGluProSerLysAlaLeuLysGlu         306
                            :: ::
Db 1069 GAAAAAACCAAAGGCTAACTGAAAGGATAGCCGAACCTACTAAGACTTTTTCAAG      1128

Qy  307 LysValSerThrAspThrLysAspLeuPheGluAsnLysIleGluGlyGlnGlyThrValAsp  326
           |||||| :::
Db 1129 GAGGCTCCTCAAGTACCAAACACTTCTGATGAGAACATTGGCCAACCACCAAGGAG      1188

Qy  327 PhePheAsnLysGluIleGluArgAspProSerLysValSerAsnAsp             346
           ||||| :::
Db 1189 TTTTTCAGGAAGCTCCCCAAGCCACTAAACATTTCCTAGACGAAAACATCGGTCAACCA  1248

Qy  347 AlaLysAspLeuPheGluAsnGlyIleGlyGlnGlyThrValAspPheIleAsnAsnGlu  366
           |||||
Db 1543 ACTGTTGGCCAACCTACAAAGGAGTTTTTCAGAAGAATTCCTGAACGGAGCTTTAGAAAACTACTAAAGACGCA  1602
```

Based on the right column (additional alignment blocks and GenBank record):

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Db 1249 ACCAAGGAGTTCTTC---AGGGAGGCGTCCTCAAGCCACTAAGCACTTCCTAGGCGAGAAT  1305
           |||   :::       :::    |||           |||              |||::
Qy  367 IleArgAspProSerLysAlaLeuArgGluLysValSerValSerThrGlyAlaGluAlaSerProLeuPhe  386

Db 1306 ATTGCTCAACCTACTAAAGAAAGTTTCAAGGATGTCCCTCAAGTCACCAAGAAAGTTATA  1365
           |||::||||                    :::      |||
Qy  387 GluAsnLysIleGlyGlnGlyThrValAspPhe------------------------     397

Db 1366 ACTGAGAACAATTGCTCAACCAACTAAGGAGAGTTCCTCAGAGGAGGTTCCTCATGTCCAGATG  1425
                 |||    ::::||       |||                  |||
Qy  398 ------IleAsnAsnGluIleGluArgAspProSerLysAlaLeuArgGluLysValTyrThr  415

Db 1426 AAAGTCTTGAATGAAAACATTGCTCAACCTCCAAAAGGAAATCATACATGGAGTTTGGTACA  1485
           :::|||||||||           |||
Qy  416 GluLeuAlaAspLeuProPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnLys  435

Db 1486 GGCGGCCAAGAAT---TTCATTCCCGAGCCCATGAAGGTACTGAAGTTGCTTAAAACGAA  1542
           |||       ::: ---      |||                    ||:::
Qy  436 GluIleGluArgAspProSerLysAlaLeuGlnIleArg-----LysValSerValSerThrGlyGluIleAlaAspAsn  454

Db 1603 TTA                                                         1605
           |||
Qy  455 Leu                                                         455
```

RESULT 15

AF030059

LOCUS   AF030059   2325 bp   DNA   linear   INV 13-NOV-1997

DEFINITION   Babesia bovis strain T2b rhoptry associated protein-1 (rap-1) gene, complete cds.

ACCESSION   AF030059

VERSION   AF030059.1   GI:2613064

KEYWORDS   .

SOURCE   Babesia bovis.

ORGANISM   Babesia bovis
    Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.

REFERENCE   1 (bases 1 to 2325)
   AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
   TITLE   Structure, sequence, and transcriptional analysis of the Babesia bovis rap-1 multigene locus
   JOURNAL   Unpublished

REFERENCE   2 (bases 1 to 2325)
   AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
   TITLE   Direct Submission
   JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology, washington State University, Pullman, WA 99164, USA

FEATURES   Location/Qualifiers
   source   1..2325
       /organism="Babesia bovis"
       /strain="T2b"
       /db_xref="taxon:5865"
       /note="isolated in Texas, USA"
   gene   22..1719
       /gene="rap-1"
       /note="gene copy 1"
   CDS   22..1719
       /gene="rap-1"
       /codon_start=1
       /product="rhoptry associated protein-1"
       /protein_id="AAB84269.1"
       /db_xref="GI:2613065"
       /translation="MRIISGVVGCLFVFSHHVSAFRHNQRVRGVSLAPAEVVGDLTSTL
ETADFLMTLRDHMHNITIKDMKHVLSNGREQIVNDVCSNAPEDSNCREVNVNNYADRCEM
YGCFFIDNVKYPLYQEYVQPLSIPNPYQLDAAFRLFKESASNPAKNSVKREWLRFRNGA
NHGDYHYFVTGLLNNNVHEEGTTDVEYLVNKVLYLMATMNYKTYLTLTVNSNMAKFENRF
SFTIKIFSRRIRQTLSDIIRWNVEDFEFDEERSIERITTQLFSSYEDYMLTQIPTLSKFAR
RYADWVKKVLLGSTTSYVEAPWYKRWIKKFRPDFSKNVTQPTKKFFEDINEVTKNYLK
ANVAEPTKMAKRPMQDTHEKTKGYLKENVAEPTKTKFFKEAPQVTKHFEDENIGQPTKEFFR
EAPQATKHFLDENIGQPTKEFFRERAPQATKHFLGENIAQPTKEFFKEEPFKIEDTNEVTKIVTE
NIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTAKNFISAAHEGTKQFLNET"

BASE COUNT   763 a   473 c   445 g   644 t

ORIGIN

US-09-807-459-2 (1-458) x AF030059 (1-2325)

Alignment Scores:

Pred. No.:   1.04e-57
Score: 826.50
Percent Similarity: 51.30%
Best Local Similarity: 35.53%
Query Match: 35.04%

Length: 2325
Matches: 178
Conservative: 79
Mismatches: 195
Indels: 49
Gaps: 6

VGQPTKEEFLNGALETTKDALHHLGKSSEEANLYDATENTTQANDSTTSNGEDTAGYL"

Qy   1   MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer   20
         :::||||||||||||||||::::::
Db   1   CTCGCTCCAGCTGAACTGGTGAGGTGGTTAACCTCCACATTGGAAACAGCTGATACTTTG   171

Qy   21 ValAspSerAlaAlaAsnAlaThrTyrMetIleAsnSerAsnAspTyrLeuSerAla   40
         ::: ||| :::
Db 112 ATGACTCTCCGTGACCACATCCACACAACATTACTAAGGATATGAAAACATGTTTTGAGCAAT 231

Qy   41 ValSerAspAsnPheAlaGlyLeuArgIleCysSerGlnValProLysGlySerAsnCysSer   60
         :::
Db 232 GGTCGTCTGAGCAGAGATGTAAAATGTGTTGCTCTAATGCCTCCCAAACTGTCGT   291

Qy   61 AlaSerValSerAlaThrTyrMetSerArgCysAlaLysGlnAspCysCysLeuThrLeuGlnSer   80
         |||:::|||
Db 292 GAGGTAGTTAACAAATTATGCGACCGTTGTGAAATGTTACGGAGATGCTTTACGATTGACAAT   351

Qy   81 LeuLysTyrTyrProLeuGluAlaLysTyrGlnProLeuProAspProTyrGlnLeu   100
         :::|||
Db 352 GTCAAATATCCGTTGTATCAAGAGTACCAACCTCTATCTCCTTCCAAACCTTACCAGTTG   411

Qy 101 GluAlaAlaPheIleLeuPheLysGlyLeuSerAspAlaAsnProAlaAsnSerThrArgLeuLys   120
         :::||||||:::
Db 412 GATGTCTGCGGTTCAGATGTTCAGAAATGGAGCGAAGAGTGCATCGAACCCTTGCCAAGAACAGCGTAAA   471

Qy 121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrTyrPheHisAspLeuValPhe   140
         |||||||||:::
Db 472 CGCGAAATGGTTCGCGTTCAGAAATGGAGCGAAGAGTGCATCGAACCCTTGCCAAGAACAGCGTAAA   531

Qy 141 AsnLeuLeuGluLysGluArgAspAlaAlaSerAlaThrAspIleGluLeuAsnPheAla   160
         :::|||||||:::
Db 532 GGTCGTCTTGAACAACAATGTTGTGCACGAGGAAGGAAACTACCGATGTTGAAATATCTTGTC   591

Qy 161 SerArgTyrLeuThrTyrMetAlaThrLeuThrTyrTyrLysThrTyrThrArgAsnValAspGluPhe   180
         |||:::
Db 592 AACAAGTTACTCTATATGGGCTACCATTGAACTACAAGACTTATTTGACAGTAAAACGTATG   651

Qy 181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLys   200
         |||
Db 652 AACGCCAAGTTCTTCAACAGAATTCAGCTTCACTACAAGATATTCAGTCGTCGTATTAGG   711

Qy 201 ArgAlaLeuLysPheAlaLysSerGlnIleIleIleGluArgSerAsnLeuProLeuAspIleGlyThrHisSer   220
         :::|||||| |||:::
Db 712 CAAACAATTGAGTGATATCATCAGGTGGAAGTGTTCCTGAAGATTTT--GAAGAAAGGAGC   768

Qy 221 ValSerArgLeuGlnHisIleThrSerSerThrTyrLysAspThrTyrMetAspThrGlnIlePro   240
         ::: |||:::
Db 769 ATCGAACGTATCACTCAACTTACTACGCAGTTACGAGAGATTACAGTGTTGACCCAGATTCCA   828

Qy 241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuAlaThr   260
         ||| |||:::
Db 829 ACTCTTTCCAAGTTTCCACGCTCGTTATGCGACAGGTTGAAAGGTTCTGCGGTAGC   888

Qy 261 ValAlaGlyTyrValAspThrProThrPtyTyrLysLysTrpTyrMetLysLeuLysAsnPhe   280
         ::: |||:::
Db 889 TTGACCTCGTACGTTGAAGCTCCTTGGTACAAAAAGATGGATAAAGAAATTCAGAGATTTT   948

Qy 281 MetValAsnArgValPheIleProThrHisLysLysPhe   292
         |||
Db 949 TTCTCTAAAAAACGTTACCCAACCTACAAAAGAAGTTCATCGAGGATACTAACGAAGTTACC   1008

Qy 292 --   292
Db 1009 AAAAAACTATCTGAAAGCCAATGTTGTCTGAGCCCCACTAAAAAGTTATGCAGGAGACACTCAC   1068

Qy 293 -----------PheAsnLysGluIleArgGluProSerLysLysAlaLeuLysGlu   306
                    ::: ||||||||:::|||
Db 1069 GAAAAAAACCAAAAGCCTATCTGAAGACAAGATAGCCGAACCTACTAAGACTTTTTTCAAG   1128

Qy 307 LysValSerThrHrAspThrLysAspLeuPheGluAsnLysLysIleGlyGlnGlyThrValAsp   326
         ||||||| |||:::
Db 1129 GAGGCGTCCCAGTCACCAAAACACTTCTTCGATGAGAACAATTGGCCAACCCAACCAAGGAG   1188

Qy 327 PhePheAsnLysGluIleLeuArgAspProSerLysLysAlaLeuLysGluIleLysValSerSerAsnAsp   346
         |||||| :::|||
Db 1189 TTTTTCAGGGAAGGCTCCCCAAGCCACTAAAACATTCCTAGACGAAAAACATCGGTCAACCA   1248

Qy 347 AlaLysAspLeuPheGluAsnLysLysIleGlyGlnGlyThrValAspPheIleAsnAsnGlu   366
         ||||||:::|||
Db 1249 ACCAAGGAGTTCTTC---AGGGAGGCGTCTCAAGCCACTAAGACACTTCTTAGGGGAGAAT   1305

Qy 367 IleLeuArgAspProSerLysLysAlaLeuLysGluIleLysValSerSerAsnLys   386
         |||:::
Db 1306 ATTGCTCAACTACTAAAAAAGAATTTTTCAGGATGTCCCTCAAGTGCACCAAGAAGGTTATA   1365

Qy 387 GluAsnLysIleGlyGlnGlyThrValAspPhe---------------------   397
         |||:::
Db 1366 ACTGAGAACAATTGCTCAACAACTAAGAACATTCCTCATTGCTAGGATATGGGGTTTATA   1425

Qy 398 ------IleAsnAsnGluIleLeuArgAspProSerLysLysAlaLeuLysGluIleLysValSerValTyrThr   415
               :::|||
Db 1426 AAAGTCTTCAAGTGAATGAAAACATTGCTCAAACCTGCCAAGACGTTCCTAGGGGAGAAT   1485

Qy 416 GluLeuAlaAspAspProLeuPheGluAsnLysLysIleGlyGlnGlyThrValAspPheIleAsnLys   435
         :::|||
Db 1486 GGGCCGCCAAGAAT---TTCATTTCCGCAGCCCATGAAGGTACTAACCAGTTGCTTAAACGAA   1542

Qy 436 GluIleLeuArgAspProSerLysLysAlaLeuLysGluIleArg---LysValSerThrGluAlaAspAsn   454
         :::|||
Db 1543 ACTGTTGGCCAACCTACAAAAGGAGAGCGTTTAGAAAACTACTAAGAAGACGGCA   1602

Qy 455 Leu 455
         |||
Db 1603 TTA 1605

RESULT 16
AF030056

LOCUS   AF030056   2385 bp   DNA   linear   INV 13-NOV-1997
DEFINITION   Babesia bovis strain S2P rhoptry associated protein-1 (rap-1) gene,
             complete cds.
ACCESSION   AF030056
VERSION   AF030056.1 GI:2613058
KEYWORDS   .
SOURCE   Babesia bovis.
  ORGANISM   Babesia bovis
             Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
             Babesia.
REFERENCE   1 (bases 1 to 2385)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE   Structure, sequence, and transcriptional analysis of the Babesia
             bovis rap-1 multigene locus
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 2385)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
             Washington State University, Pullman, WA 99164, USA
FEATURES   Location/Qualifiers
     source   1..2385
                     /organism="Babesia bovis"
                     /strain="S2P"
                     /db_xref="taxon:5865"
                     /note="isolated in Argentina"

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                /note="gene copy 1"
CDS             87..1784
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                /protein_id="AAB84266.1"
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                NHGDYHYFVTGLLNNNVVHEEGTDVEYLVNKVLYMATMNYKTYLTVNSMNAKFFNRF
                SFTKIFSRRIRQTLSDIIRWNVPEDFEERSIERITLQLSSYEDVMLTQIPTLSKPAR
                RYADMVKKVLLGSLTSYVEAPWYKRWIKKRDFEFSKNVTQPTKHFFDENIGQPTKEFFR
                ANVAEPTKTFPFKEAPQVTKHFFDENIGQPTKEFFR
                EAPQATKHFLDENIGQPTKEFFREAPQVTKHFLGENIAQPTKEFFKDVPQVTKVITE
                NIAQPTKEFLREVPHATKMKVLNENIAQPAKEIIHEFGTGAKNFISAAHEGTKQFLNET
                VGQPTKEFLNGALETTKDALHHLGKSSEEANLYDATENTTQANDSTTSNGEDTAGYL"

BASE COUNT      772 a   492 c   465 g   655 t   1 others
ORIGIN
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Alignment Scores:

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Pred. No.:              1
Score:                  1.07e-57
Score:                  826.50
Percent Similarity:     51.30%
Best Local Similarity:  35.53%
Query Match:            35.04%
DB:

US-09-807-459-2 (1-458) x AF030056 (1-2385)

Length:       2385
Matches:      178
Conservative:  79
Mismatches:   195
Indels:        49
Gaps:           6
```

```
Qy    1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer 20
          :||||||    |:||    |||||||||||
Db    1 CTCGCTCCACCTGAAGTGGTGAGTGATTTAACCTCCACATTGGAAACAGCTGATACTTTG 177

Qy   21 ValAspSerAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla 40
          |||        :|     |||
Db  177 ATGACTCTCCGTGACCACATGACAAACATTACTAAGGATATGAAACAGTTTTGAGACAAT 237

Qy   41 ValSerAspAsnProHisAlaGluArgIleCysSerSerGlnValProLysGlySerCysSer 60
          :||||||   ::||
Db  297 GGTCGTGAGCAGGATTGTAAATGATGTTTGCGTCTCTAATGCTCCTCAACTCGT 297

Qy   61 AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
          :||||||    ||||:
Db  357 GAGGTAGTTAACAATTATGCTGACCGTTGTGAAATGTACGGATGCTTTACGATTGACAAT 416

Qy   81 LeuLysTyrProLeuGlnAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu 100
          :::::
Db  417 GTCAAAATACCGGTTGTATCAAGAGTACCAACCTCTATCTCTTCAAAACCCTTACCATG 477

Qy  101 GluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys 120
          ||:      ||||||||||:   ::|||
Db  477 GATCCTGCGTTCAGATTGTTCAAAGAGAGTCATCGAACCCTGCCAAACAGCGTAAAA 536

Qy  121 ArgPheThrMetArgPheArgArgGlyLeuValPheHisHisSerThrTyrPheHisAspLeuValPhe 140
          ||:      ||||||||||:   ::|||
Db  537 CGCGAAATGGTTGCGTTTCAGAAATGGAGCCGAACCATGGTGATTACCACTACTTCGTCACT 596

Qy  141 AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrArgAspIleGluAsnPheAla 160
          |||||||    :::
Db  597 GGTCGTCGTCAAACAAATGTTGTCACGAGGAGAACTACCGATGTGAAATATCTTGTC 656

Qy  161 SerArgTyrLeueuTyrMetAlaThrLeuThrTyrTyrLysThrTyrThrAsnValAspGluPhe 180
          :||||||||:::|||    ||||||||||
Db  657 AACAAGGTACTCTATATGGCTACCACAGAACTATTACCAAGAGACTTAAACAGTATG 716

Qy  181 GlyValAlaSerPheAsnLysLeuSerPheThrThrArgGlyLeuPheGlyIleLeuLys 200
          |||    ||    :|||||||||:   ::|||
Db  717 AACCCCAAGTTCTTCAACAGATTCAGCTTCACTACAAAGAGTATTCAGTTGGTAGG 776

Qy  201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSer 220
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Db  201 ...
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Db  777 CAAACATTGAGTGATATCATCAGGTGGAATGTTCCTGAGGATTTT---GAAGAAAGGAGC 833
Qy  221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro 240
          |||||||||||:|||    |||
Db  834 ATCGAACGTATCACATCAAGCTTACTACAGAGCATACAGAGATTACACATGTTGACCAGA 893

Qy  241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
          ||||||||||||:||    :::
Db  894 ACTCTTCCAAGTTTGCACGTCGTTTATCCTGACAATGGTGAAGGTTCGTCAAGGTAGC 953

Qy  261 ValAlaGlyThrValAlaAspThrProThrPheTyrLysTyrMetLysLeuLysAsnPhe 280
          :::||    :|||||||||||:|||
Db  954 TTGACCTCGTACGTTGAAGCTCTTGGTGACAAAGATGGATAAAAGAATTCAGAGACTTT 1013

Qy  281 MetValAsnArgValPheIleProThrThrLysLysPhe------ 292
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Db 1014 TTCTCTAAAAACGTTACCCAACCTACAAAAGAGTTCATCGAGGATACTGACGAAGTTACC 1073

Qy  292 ------ 292
          :::
Db 1074 AAAAACATATCTGAAAGCCAATGTTGCTGAGCCCACTAAAAAGTTTATGCAGGACACTCAC 1133

Qy  293 ------ 293
          :::
Db 1134 GAAAAAACCAAAGAGCTATCTGAAGAGAATTGGCCGAACAACTTACTAGACAGTTTTTCGAGAAT 1193

Qy  307 LysValSerThrArgAspThrAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp 326
          |||    :::
Db 1194 GAGGCTCCTCAAGTCACCAAAACACTTCTTCGATGAGAACATTGGCCAACCCACCAAGGAG 1253

Qy  327 PhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAsp 346
          ||||||    ::|
Db 1254 TTTTTCAGGGAAGCTCGCGACCCACTAAACATTTCCTAGACGAAAAACATCGGTCAACCA 1313

Qy  347 AlaLeuLysAspLeuPheGluAsnLysIleGlyGlyThrValAspThrProLysLysGlu 366
          |||    :::
Db 1314 ACCAAGGAGTTCTTC---AGGGAGGCTCCTCAAGCCACTAAGCACTTCTTAGGCGAGAAT 1370

Qy  367 IleArgAspProSerLysAlaLeuLeuIleArgGlyValSerThrGlyAlaGluAspLeuPhe 386
          |||    ::|||
Db 1371 ATTGGTCAAACCTACTAAAGAGTTTTCAAGGATGTCCCTCAAGTCACCAAGAAGGTTATA 1430

Qy  387 GluAsnLysIleGlyLysGlyThrValAspPhe------ 397
          |||    |||
Db 1431 ACTGAGAACATTGCTCAACCAACTAAGGAGTTCCTCATCGTACCATG 1490

Qy  398 ------IleAsnAsnGluIleArgAspProSerLysAlaLeuLeuIleArgLysValThrTyrThr 415
          :::    |||
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Qy  416 GluLeuArgAspProSerLysLeuIleGlyGlyThrValAspPheAsnLys 435
          |||    :::
Db 1551 GGCGCCAAGAAT---TTCATTTCCGCAGCCCATGAAGGTACTAAGCAGGAA 1607

Qy  436 GluIleArgAspProSerLysAlaLeuIleLeuArg---LysValSerThrGlyAlaAspAsn 454
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Db 1608 ACTGTTGGCCAACCTACAAAGGAGAATTCCGACGGAGCTTTAGAAACTACTAAAGAGACCA 1667

Qy  455 Leu 455
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Db 1668 TTA 1670
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RESULT 17
AF027149
AF027149

LOCUS       AF027149   11184 bp   DNA   linear   INV 24-JUL-1998
DEFINITION  Babesia bovis phosphomannomutase homolog (pmm), rhoptry associated
            protein-1 (rap-1) allele 1, rhoptry associated protein-1 (rap-1)
            allele 2, and DnaJ homolog genes, complete cds.
ACCESSION   AF027149
VERSION     AF027149.1  GI:2731569
KEYWORDS    .
SOURCE      Babesia bovis.
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ORGANISM  Babesia bovis
          Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
          Babesia.
REFERENCE   1 (bases 1 to 11184)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE     Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
  JOURNAL   Mol. Biochem. Parasitol. 93 (2), 215-224 (1998)
  MEDLINE   98327208
REFERENCE   2 (bases 1 to 11184)
  AUTHORS   Suarez,C.E., Palmer,G.H. and McElwain,T.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-SEP-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164-7040, USA
FEATURES             Location/Qualifiers
     source          1..11184
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                     /strain="Mexico Mo7"
                     /db_xref="taxon:5865"
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                     951..1028,1063..>1170)
                     /gene="pmm"
                     /product="phosphomannomutase homolog"
     gene            join(53..109,166..280,315..391,427..518,660..873,
                     951..1028,1063..1170)
                     /gene="pmm"
     CDS             join(53..109,166..280,315..391,427..518,660..873,
                     951..1028,1063..1170)
                     /gene="pmm"
                     /codon_start=1
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                     /db_xref="GI:2731570"
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                     RYIADLDIPTKRGTFIEHRKSLINICPPGRNCSMVDRRFVEYDSTHHVRQKLIQVLK
                     SQFDSDDCPLSFVAGGQISIDVYPKAWSKSIALSHIGKCDVIHFGDNTREGGNDFEI
                     YNHPDVIGHTVTGYKDLVNQLEELLAKS"
     mRNA            join(<7748..7959,8018..8123,8159..8206,8240..>8872)
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                     /product="rhoptry associated protein-1"
                     /evidence=experimental
     gene            <2302..>3999
                     /gene="rap-1"
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                     /gene="rap-1"
                     /product="rhoptry associated protein-1"
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     gene            2302..3999
                     /gene="rap-1"
                     /allele="1"
     CDS             2302..3999
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                     /allele="1"
                     /codon_start=1
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                     /db_xref="GI:2731571"
                     /translation="MRIISGVVGCLFLVFSHHVSAFRHNQRVGSLAPAEVVGDLTSTL
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     CDS             join(9640..9666,9701..10900)
                     /note="putative Hsp40"
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                     /translation="MPHHRSREVDNEKFYKVLGLSRDCSESEIKAYRKLAIKHHPD
                     KGDSEMPKEITRAYEVLSDPEKRRIYDEAGEDGLEGNMPHGDPDSIDFDLFFGGGRKP
                     KKKRGRGDVVTQLKVTLEQIYNGAMRKLAINKDVVCDDCDGTGGDSAFVSCDLCNGR
                     GIRVQIRQMGAMIQQSOSMCHACNGQGRSINESRKCKCSGKGVWQMKKILEVNIDRG
                     VPDQHKVTFHGEADERPNEIPGNVVFIICQAPHDQFKRSGSDLLIVKQLQYEALTGA
                     VYIKHLDGRVLRIIQTPANEVIRPSSIFVIENGGMPVYQSAFEGKGNLVVNFEVQFPVS
                     RKFSAAAEKDQLKSLFPYKPESKPSGTTAAENVDAREVDPQEIHDRAHAQSQQQADSDR
                     EDHHHHEGRSSVQCNQQ"
     mRNA            join(<7748..7959,8018..8123,8159..8206,8240..>8872)
                     /product="similar to ORF YJR070C from S. cerevisiae"
     CDS             join(7748..7959,8018..8123,8159..8206,8240..8872)
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                     /note="similar to ORF YJR070C from S. cerevisiae"
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                     /translation="MADLATAIAEFDSLNEFSKRPDAKLLSTILLSDGVKLSQQLKALY
                     FCRDLSSSECATILKKALEVHYDTFLRHEIAVYIGQAECEEAADVLVRLLEDTNEDPM
                     VRHEAAKAIAAIGDKTYIDKLEKVKDDSIVVRDTCRLALESLNNNAKKGDSDGVAI
                     CGCVSAPISTSAYRAIDPVPCVATEIAEMSILELNKVMLDESAPLHKRYEALYQIRNS
                     GGDEAAVWIGNALLISDNVSEVFRHECARVLGQMQSMAAADHLLKCLSNSQEKPIARHE
                     AALALGSCAAASNNQSDRNRIIAALEAHKLDSMKVVADSCIVALDVISESAIEAAS"
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                     /gene="rap-1"
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     mRNA            <5180..>5877
                     /gene="rap-1"
                     /product="rhoptry associated protein-1"
     CDS             5180..5877
                     /gene="rap-1"
                     /allele="2"
                     /codon_start=1
                     /product="rhoptry associated protein-1"
                     /protein_id="AAC27387.1"
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                     /translation="MRIISGVVGCLFLVFSHHVSAFRHNQRVGSLAPAEVVGDLTSTL
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BASE COUNT     3526 a   2046 c   2194 g   3418 t
ORIGIN
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Alignment Scores:
Pred. No.:
Score:                  6.95e-57
Pred. No.:              1
Score:                  826.50
Percent Similarity:     51.30%
Best Local Similarity:  35.53%
Query Match:            35.04%

Length:                 11184
Matches:                178
Conservative:           79
Mismatches:             195
Indels:                 49
Gaps:                   6
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US-09-807-459-2 (1-458) x AF027149 (1-11184)

Qy    1 MetAlaProSerAspSerAlaValGlyAspValThrLeuLeuAlaLeuAlaSerGluSer  20
          |:|||||||:::::
Db 2392 CTCGCTCCAGCTGAAGTGGTAGGTGATTTAACCTCCACATTGGAAACAGCTGATACTTTG 2451

Qy   21 ValAspSerAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla  40
            |:||   |||
Db 2452 ATGACTCTCCGTGACCACATGCACAACATTACTAAGGATATGAAACATGTTTTGAGCAAT 2511

Qy   41 ValSerAspAsnPheAlaGluArgIleCysSerGlnIleValProLysGlySerAsnCys  60
          |||||:
Db 2512 GGTCGTGACAGATTGTAAATGAGTGTTTGCTCTAATGCTCCTGAGGACTCCAACTTGCGT 2571

Qy   61 AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer  80
          |||::
Db 2572 GAGGTAGTTAACAAATTATGCTGACCGGTTGTGAAATGTAGCGGATGCTTTACGAATGACAAT 2631

Qy   81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu 100
          :||||||||
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YGCFTIDNVKYPLYQEYQPLSLPNPYQLDAAFRLFKESASNPAKNSVKREWLRFRNGA
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NIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKNFISAAHEGTKQFLNET
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Qy    2632 GTCAAATATCCGGTTGTATCAAAGAGTACCAACCTCTATCTCTTCAAAACCCTTACCAGTTG 2691
           |||||||                                                ||||||
Db     101 GATCCTGCGTTCAGATTGTTCAAAGAGAGTGCATGCAACCCTGCCAAGACAGCGGTAAA 2751

Qy     101 GluAlaAlaAlaPheIleLeuPheLysGluSerAspProAlaAsnSerThrGluLys 120
           ::::::  |||||||||||  :::::  ||||||||||  :::
Db     101 GluAlaAlaAlaPheIleLeuPheLysGluSerAspProAlaAsnSerThrGluLys 120

Qy    2692 GATCCTGCGTTCAGATTGTTCAAAGAGAGTGCATGCAACCCTGCCAAGACAGCGGTAAA 2751

Qy     121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
           |||                      :::           |||
Db    2752 CGGCAAATGGTTCGCGTTCAGAAATGGAGCGAACCCATGGTGGATTACCACTACTCGTCACT 2811

Qy     141 AsnLeuLeuGlyLysAsnValThrArgAspAlaAspAlaIleThrAspPheAla 160
           :::                      |||:::::           |||
Db    2812 GGGTCTGTTGAACAACAAATGTTGTCCACGAGGAAGGAACCTACCGGATGTTGAATATCTTGTC 2871

Qy     161 SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPhe 180
           :::                      |||:::::           |||
Db    2872 AACAAGGTACTCTATATGGCCACACTATATTATAAGACTTATTACAGTAAACAGTATG 2931

Qy     181 GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyTyrIleLys 200
           |||   ||||||||                      :::||
Db    2932 AACGCCAAGTTCTTCAACAACAGATTCAGCTTCACTACAGGACTATTCGGTTGGGGTTATAGG 2991

Qy     201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSer 220
           :::                      ||||||           |||
Db    2992 CAAAACATTGAGTGATATCATCAGGTGGAAGTGTTCCTGAAGAATTTT---GAAGAAAGGAGC 3048

Qy     221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro 240
           |||:::   ||||||||                      |||
Db    3049 ATCGAACGTTATCACTCAACTTACTACGAGAATTACATGGACACGCAGAATTCCA 3108

Qy     241 AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnAsnGlyLeuLeuAlaThr 260
           |||   ||||||||                      :::|||
Db    3109 ACTCTTTCCAAGTTTGCACGTCGTTTATGCTGACATGGTGAAGAAGGTTCTGCTCGGTAGC 3168

Qy     261 ValAlaAlaGlyTyrValAspThrProThrProThrTyrLysLysTrpIleTyrMetGlyLeuValAsnPhe 280
           |||:::           |||:::::::||
Db    3169 TTGACCTCGTACGTTGAACCCTTGGTACAAAAGATGGATAAAAGAAATTCAGAGAATTTT 3228

Qy     281 MetValAsnArgValPheIleLeuProThrLysLysSerPhe--------------- 292
           |||
Db    3229 TTCTCTAAAAACGTTACCCAACCTACAAAGAAGTTCATCCGAGGATACTAACGAACGTTACC 3288

Qy     292 --------------------------------- 292
Db    3289 AAAAACTATCTGAAAGCCAATGTTCGCTGAGCCCACTAAAAAGTTATGCAGGACACTCAC 3348

Qy     293 ---------PheAsnLysGlyIleIleArgGluProSerLysLysGlu 306
Db    3349 GAAAAAACCAAAGCTACTGAAAGAAGAATGTAGCCGAACCTACTAAGACTTTTTCAAG 3408

Qy     307 LysSerValSerThrArgAspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp 326
           :::                      :::|||
Db    3409 GAGGCTCCTCAAGTCACCAAAACACTTCTTCGATGAGAACATTGGCAACCCACCAAGGAG 3468

Qy     327 PhePheAsnLysGluIleLeuArgAspProSerLysAlaLeuLysGlyLysValSerAsnAsp 346
           |||||||                      |||:::
Db    3469 TTTTTCAGGGAAGCTCCCAAGGCACTAAAACATTTCCTAGACGAAAAACATCGGTCAACCA 3528

Qy     347 AlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGlu 366
           :::                      |||:::
Db    3529 ACCAAGGAGTTCTTC---AGGGAGGCTCCTCAAGCACTTCCTAAGACTCCTAAGGAAAT 3585

Qy     367 IleArgAspProSerLysAlaLeuIleLeuArgGlyValAlaGluAspLeuPhe 386
           :::                      ::::::|||
Db    3586 ATTGCTCAACCTACTAAAGAATTTTCAAGAATGTCCCTCAAGTCACCAAGAAGGTTATA 3645

Qy     387 GluAsnLysIleGlyGlnGlyThrValAspPhe--------------- 397
           |||                      |||
Db    3646 ACTGAGAACATTGCTCAACCAACTAAAGAGTTCCTTAGGGAGGTTCCTCATGCTACCATG 3705

Qy     398 ------IleAsnAsnGluIleArgAspProSerLysAlaLeuIleLeuArgGlyValTyrThr 415
           |||                      :::|||
Db    3706 AAAGTCTTGAATGAAAAACATTGCTCAACCTGCCAAGGAAAATCATACAGAGTTGGTACA 3765

Qy     416 GluAlaAlaAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIleAsnLys 435
           |||   :::                      :::|||
Db    3766 GCGCGCAAGAAAT---TTCATTTCCGACAGCCCATGAAAGGTACTAAGCAGTTCTTAAACGAA 3822

Qy     436 GluIleArgAspProSerLysAlaLeuIleLeuArg---LysValSerThrArgGluAlaAlaAspAsn 454
           :::                      :::|||
Db    3823 ACTGTTGGCCAACCTACAAAGAAGAATTCCTGACGGACTTTAGAAACTACTAAAGACGCA 3882

Qy     455 Leu 455
           |||
Db    3883 TTA 3885
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RESULT 18
AF030062
LOCUS   AF030062   2325 bp   DNA   linear   INV 13-NOV-1997
DEFINITION Babesia bovis strain R1A rhoptry associated protein-1 (rap-1) gene,
            complete cds.
ACCESSION   AF030062
VERSION   AF030062.1 GI:2613070
KEYWORDS   .
SOURCE   Babesia bovis.
  ORGANISM Babesia bovis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 2325)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE   Structure, sequence, and transcriptional analysis of the Babesia
            bovis rap-1 multigene locus
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 2325)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hotzel,I. and McElwain,T.F.
  TITLE   Direct Submission
  JOURNAL   Submitted (17-OCT-1997) Veterinary Microbiology and Pathology,
            Washington State University, Pullman, WA 99164, USA
FEATURES   Location/Qualifiers
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                     SFTTKIFSRRIRQTLSDIIRNVPEDFEERSIERIIQLTSSYDYMLTQIPTLSKFAR
                     RYADMWKRVVLLGSLTSYVEAPWYKRWIKKFRDFFFSKNVTQPFKKFIEDTNEVTKNVLK
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BASE COUNT   766 a   477 c   437 g   642 t   3 others
ORIGIN

Alignment Scores:
Pred. No.:   1.25e-57
Score: 825.50   Length: 2325
Percent Similarity: 51.908   Matches: 183
Best Local Similarity: 36.538   Conservative: 77
Query Match: 34.998   Mismatches: 192
DB: Indels: 49
                                                     Gaps: 8

US-09-807-459-2 (1-458) x AF030062 (1-2325)

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Qy      1 MetAlaProSerAspSerValGlyAspValThrLeuThrLeuLeuAlaAlaSerGluSer 20
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Db    112 CTCGCTCCAGCTGAGCTGGTAGGTGGTTGATTTTAACCTCCACATTGGAAACAGCTGA 171

Qy     21 ValAspSerAlaAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla 40
            ::   ||||||  |||| |::||||||
Db    172 ATGACTCTCCGTGACCACATGCACAACATTACTAAGGATATGAAACATGTTTGAGCAAT 231

Qy     41 ValSerAspAsnPheAlaGluArgIleCysSerSerGlnValProLysGlySerAsnCysSer 60
            |||||||||||  :::|||  |||||
Db    232 GGGCGGTGAGCAGATTGTAAATGATGTTTTGCCTCTAATGCCTCGAGGACTCCAACGTCGT 291

Qy     61 AlaSerValSerAlaThrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
            |||:||  ||||  |||::||
Db    292 GAGGTAGTTAACAATTATGCCGACCGTTGTGAAAATGACCGGATGCTTTACGATTGACAAT 351

Qy     81 LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAlaProProTyrGlnLeu 100
            :||:::|||||  :||||||||||||
Db    352 GTCAAATAATCCGTTGTATCGAAGAGTACCAAACCCTATCCTTCCAAACCCTTACCAGTTG 411

Qy    101 GluAlaAlaAlaPheIleLeuPheLysGluSerAspAlaAlaAsnSerThrGlyLys 120
            :||  ||||||||||||||
Db    412 GATGCTGCGTTCAGATTGTTCAAAGAGAGTGCATCCAACCTCTACTTCCAGTCAAAA 471

Qy    121 ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
            |||  :||:||||||||||  |||
Db    472 CGCGAAATGGTTCGCGTTCAGAAATGGAGCCAAACCATGGTTGATTACCACTACTTCCTCACT 531

Qy    141 AsnLeuLeuGluLysAsnValThrArgAspAlaAlaThrArgPheGluAsnPheAla 160
            ||||||  ||||
Db    532 GGTGTCGTTGAACAACAATGTTGTGTCCACGGGGAAGGAAGCAACTACCGAtGTTGAAATATGTTGTC 591

Qy    161 SerArgTyrLeuTyrMetAlaThrLeuThrTyrThrTyrLysThrTyrThrAsnValAspGluPhe 180
            :::|||  ||||||||||  ||||||||
Db    592 AACAAGGTACTCTATATGGCTACCATGAACTACAAGACTTATTCAACAGTATG 651

Qy    181 GlyAlaSerPheArgPheAsnLysSerPheThrThrArgGlyTrpGlyIleLys 200
            ||||||||||  ||::::
Db    652 AACGCCAAGTTTTTCAACAGAATTCAGCTTCACTACAAAGATATTCAGCCCTCGTATTAGG 711

Qy    201 ArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGluHisSer 220
            :::  ||||  |||  ||||
Db    712 CAAACATTGAGTGATATCATCAGGTGGGAAtGTTCCTGAAGAtTTT--GAAGAAAGGAGC 768

Qy    221 ValSerArgLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIleIlePro 240
            ||:|||||||||||||||  :::|||
Db    769 ATCGAAACGTATCACTCAACTACTACtAGCACGAGATTACATCGTTGACCAGAtTCCA 828

Qy    241 AlaLeuProLysGlySerPheSerLeuMetValGlnArgLeuLeuAlaThr 260
            ||||||||||||  :||
Db    829 ACTCTTTCCAAGTTTGCACGTCGTTTATCGTCGACAtGGTGAAGAAGGTTCGTCAGGTAGC 888

Qy    261 ValAlaLeuGlyThrValAspThrProThrTyrLysTrpTyrMetLysLeuLysAsnPhe 280
            ||||||||||  ||||:::||||
Db    889 TTGACCTCGTACGTTGAGCCTTGGTACAAAAGATGGAtTAAAGAAAttcAGAGACTTT 948

Qy    281 MetValAsnArgValPheIleLeuProThrLysLysSerPhe-------- 292
            |||
Db    949 TTCTCTAAAAACGTTACCCAACCTACAAAAGAAAGTTCATCGAGATACTAACGAAGTTACC 1008

Qy    293 ------PheAsnLysGluIleArgGluProSerLysAla------------ 303
            |||::::||||||||||
Db   1009 AAAAACTATCTGAAAGCCAATGTTTGCTGAGCCCACTAAAAAGTTTATGCAGGACACTCAC 1068

Qy    304 -------------LeuLysGlyLysValSerThrAspThrLysAspLeuPheGlu 317
            |||||||||||||||:::
Db   1069 GAAAAAAACCAAAGGCTACTCTGAAAGAGAAATGTAGCCGAACCTACTAAAGACTTTTTCAAG 1128

Qy    318 AsnLysIleGlyLnGlyThrValAspPhePheAsnLysGlyLeuArgAspProSerLys 337
            |||::::||||  |||:||
Db   1129 --GAGGCTCCTCACCAAAACACTTCTTCGAtGAGAACAATTGGCCACAACCACCAAG 1185

Qy    338 AlaLeuLysGluLysGlyValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyLnGln 357
            ||||||
Db   1186 GAGTTTTTCAGGGAAGCTCCCAAGCCCACTAAACATTCCTAGACGAAAACATCGGTCAA 1245

Qy    358 GlyThrValAsp------------------------------PheIleAsnAsnGlu 366
            ||||||||                                  |||:::|||
Db   1246 CCAACCAAGGAGtTCTTCAGGGAGGCTCCCAAGTCACtGACACTTCTTAGACGAGAAT 1305

Qy    367 IleArgAspProSerLysSerAlaLeuIleArgLysValSerThrGlyValAlaGluAspLeuPhe 386
            ||||  ||::::||||||  :::
Db   1306 ATTGCTCAACCTACTAAAGAATTTTTCAGGGAtGTCCCTCAGTCACTGACACTTCTTAGA 1365

Qy    387 GluAsnLysIleGlyLnGlyThrValAspPhe------------------------- 397
            |||  |||  :::
Db   1366 ACTGAGAACAATTGCTCAACCTACTAAAGAATTCCTTAAGGAGGTTCCTCATACTACCATG 1425

Qy    398 ------IleAsnAsnGluIleArgAspProSerLysSerAlaLeuIleArgLysValTyrThr 415
            :||||  :||||||||||||::::
Db   1426 AAAGTCTTGAATGAAAACAATTGCTCAACCTGCCAAGGAAATCAtCATACAGAGttGTTGGTACT 1485

Qy    416 GlyAlaAspAspLeuPheGluAsnLysIleGlyLnGlyThrValAspPheIleAsnLys 435
            ||||  :::|||  |||||||||
Db   1486 GGCGCCAAGAAT---TTCAtTTCCGCAGCCCATGAAGGTAGtTACTGAGGGTTCTCAtACGAA 1542

Qy    436 GluIleArgAspProSerLysAlaLeuLeuIleArg---LysValSerThrGluAlaAspAsn 454
            |||:::||||  ||||::::|||                |||   |||
Db   1543 ACTGTCTCGGCCAACCTACAAAAGGAAATTCCTGAACGAGAGTCTTAGAAAACTACTAAAGACCCA 1602

Qy    455 Leu 455
            |||
Db   1603 TTA 1605
```

RESULT 19
```
LOCUS       BBODNAA
BBODNAA
DEFINITION  Babesia bigemina DNA sequence.              2005 bp    DNA    linear   INV 26-APR-1993
ACCESSION   M85184
VERSION     M85184.1  GI:155877
KEYWORDS    .
SOURCE      Babesia bigemina (strain Mexico) merozoite DNA.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2005)
  AUTHORS   Mishra,V.S., McElwain,T.F., Dame,J.B. and Stephens,E.B.
  TITLE     Isolation, sequence and differential expression of the p58 gene
            family of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 53, 149-158 (1992)
  MEDLINE   92365724
FEATURES             Location/Qualifiers
     source          1..2005
                     /organism="Babesia bigemina"
                     /strain="Mexico"
                     /db_xref="taxon:5866"
                     /dev_stage="merozoite"
BASE COUNT      550 a    439 c    478 g    538 t
ORIGIN
```

Alignment Scores:
Pred. No.:

Score:	1.66e-57	Length:	2005
Score:	823.00	Matches:	174
Percent Similarity:	61.31%	Conservative:	78
Best Local Similarity:	42.34%	Mismatches:	129
Query Match:	34.89%	Indels:	30
DB:		Gaps:	10

US-09-807-459-2 (1-458) x BBODNAA (1-2005)

```
Qy      4 SerAspSerValGlyAspValThrLeuThrLeuLeuAlaAlaSerGluSerValAspSer 23
            :::::||||||||||||||||||||||::::||||
Db    282 GCAGAGGTGGTTGGAGAtGTGTCCAAGAGACCTTGCCTGGAAGCCAAATGAGGGTTGCAATGCT 341

Qy     24 AlaAlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
            :::||||                                                    ||| :::
Db        ||||||
```

RESULT 20

BBODNAD

```
LOCUS       BBODNAD      1962 bp    DNA     linear   INV 26-APR-1993
DEFINITION  Babesia bigemina DNA sequence.
ACCESSION   M85187
VERSION     M85187.1  GI:155880
KEYWORDS    .
SOURCE      Babesia bigemina (strain Mexico) merozoite DNA.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 1962)
  AUTHORS   Mishra,V.S., McElwain,T.F., Dame,J.B. and Stephens,E.B.
  TITLE     Isolation, sequence and differential expression of the p58 gene
            family of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 53, 149-158 (1992)
  MEDLINE   92365724
FEATURES             Location/Qualifiers
     source          1..1962
                     /organism="Babesia bigemina"
                     /strain="Mexico"
                     /db_xref="taxon:5866"
                     /dev_stage="merozoite"
BASE COUNT      502 a    447 c    498 g    515 t
ORIGIN
```

US-09-807-459-2 (1-458) x BBODNAD (1-1962)

```
Alignment Scores:
Pred. No.:
Score:                    813.50        Length:              1962
Percent Similarity:       58.66%        Matches:              180
Percent Identity:         41.57%        Conservative:          74
Best Local Similarity:    34.48%        Mismatches:           142
Query Match:                   3        Indels:                37
                                        Gaps:                  12
```

```
Qy    391 GlyGlnGlyThrValAspPheIleAsnAsnGlu 401
          |||         |||            |||::|||
Db   1431 TCACAATAATAATTCAGATCCGAAAATGATGAG 1463

Qy      4 SerAspSerValGlyAspValThrLysThrLeuLeuLeuAlaAlaSerGluSerValAspSer 23
          |||||             ||||  || |::::   :|| ||| :::    :
Db    282 GCAGAGGTGGTTGGAGATGTCCAAGACCTTCTTGCTGCAGCCAGCAGGTTGTTCAATGCT 341

Qy     24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
          |||         |||:  ||| |||       |::|           :||
Db    342 GAAATGGAAGCAGCTCAGATTAAACGAAGAATATGAAGAATTCAGTGTGGCGAACGTCAAGGAG 401

Qy     44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
          |||::         ||:  |::||| :::            |||
Db    402 ACCATCGTTGATGAGGTCTCCAGAAAAGATGCTGGAAGCCCTACGTGCCCCAAGAGCGTA 461

Qy     64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
          ||||||||:::           |||          ||||:::       :||
Db    462 ATTGCCTATCGTTGACCGTTGTGATGAGGGCCGATTGTCTGCACGCTTGACACGCATG----- 515

Qy     84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla 103
          |||||||||||||||||:::||||||||||||||||:::|||||||:||||||:||||
Db    516 -----AAGTACAACCCGTTGAGTCTGCCAAATCCTTACCAGTTGGACGCTGCC 563

Qy    104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGlyLysArgPheTrp 123
          |||||:::||||||||||||:::||||| |||            ||||||||||||
Db    564 TTCATCCTTTTCAGGGAAAGTGATTCTAACCCTGCGAAGAATGAGGTGAAGCCGCTTCTGG 623

Qy    124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu 143
          ||||||          |||||||:::|||                ||       |:::||
Db    624 ATGGCCTTCGAGG-------AGCAGCCACGGGCGACTACCAATCACTTTGTTGTTAGCTTGTTG 677

Qy    144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163
          |:::|||||||||||||||:::||| |||            ||||||:::|||:||
Db    678 AAGAGAGAATGTTGTACGCGACCCTGAATCCAAATGATGTTGAGAACTTCGCCATCGCCAGTTAC 737

Qy    164 LeuThrTyrMetAlaThrLeuThrTyrTyrThrArgAsnValAspGluProGlyAlaSer 183
          |||||||          |||        |||:::       |||||||          |||
Db    738 TTCTACAATGACTACGTTGTACTACAAGACTTACCTGACGGTTGACTTTACGGCGGGCTAAG 797

Qy    184 PhePheAsnLysSerPheThrThrGlyLeuPheGlyTrpGlyIleIleLysArgAlaLeu 203
          |||||:::       |||            ||||||||||||||||||||        |||
Db    798 TTCTTCAACAAGCTTCGTTTCAACAACTCGCCTGTTCGGGTATCCAGAAGGGCGTTG 857

Qy    204 LysGlnIleIleLeuArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSerArg 223
          ||||||||:::|||||||::: ||||||||| :::||||||       ||||||:::
Db    858 AAGCGTTGGTTAGGAGCAACCTTCCCGTTGACCTTGGAACC---CACCCTGAGGCCACC 914

Qy    224 LeuGlnHisIleThrSerSerTyrLysAspThrGlnIleProAlaLeuPro 243
          |||||:::||||||||||||||:::       |||||||||||||||||
Db    915 ATCCGACGGAAATAGCTACGGCCTACGGCCAGGTGCCTGCGATGACC 974

Qy    244 LysPheAlaLysArgPheSerLeuMetValGlnArgLeuLeuAlaThrValAlaGly 263
          |||||         |||||||       |||       ||| |||:::
Db    975 TCGTTCGCTTGGCTGAGCGTTTTCCAGATGGTACTAAGACTCTGTTTGGGTTACCGGAC 1034

Qy    264 TyrValAspThrProThrProTyrLysTyrMetLysValLysAsnPheMetValAsn 283
          |||:::|||||||||:::|||||||||:::||||||||||||||::::||||||
Db   1035 TACGTCCATTTCCCGCCGCGTACAGACAGGTACAGAAGTTCAAGGAGTTCATTGTGAAC 1094

Qy    284 ArgValPheIleProThrArgLysGlyLysPhePheAsnLysGlyGluProSerLys--- 302
          ||||||||||||       |||||||||||||:||||||:::||||||||||||||
Db   1095 ----TTCTTTACTGACCCTCGCCAAGTTGATTATCGAACCACGTCTCTCACCCTGTAAAGACT 1151

Qy    303 AlaLeuLeuLysGluLysValSerThrThrArgLysAspThrLysAsnLysIleGlyGln 322
          |||                |::   :::      ||||:::|||  ::|||
Db   1152 GCCTACACAAAGCTGTCCCGAAGAGCACAGGCTATCAGGAATGTCGTCGGTCAA 1211

Qy    323 GlyThrValAspPhePheAsnLysGluIleGluArgAspProSerLysAlaLeuLysGlyLys 342
          |||  ||||||            |||       |||  |||  ||||||||:::
Db   1212 AGCACCAAGCAATATTGCCCAC---GGTGTACGTGATTGGGCAAGATGATTAAGGAG--- 1265

Qy    343 ValSerAsnAspAlaLysAspLeuPheGluAsnLysIle---------------- 356
          ||||||||||||||:::|||            ||||||
Db   1266 ---CCTAGCCAACAAATAAATTCGTGAGAAGCTGCCTCACTACCTTTCTAAGGCA 1316

Qy    357 GlnGlyThrValAspPheIleAsnAsnGluIleLeuArgAspProSerLysAlaLeuIleArg 376
          |:::|||            |||        :::|::|||
Db   1317 AAGGGAGCAGACCGTTGAGCACGTTGTTGACAAGGTTAAA----- 1370

Qy    377 LysValSerThrGlyValGluAspLeuPheGluAsn-------------- 390
          :::||||||      |||:::|||               ||
Db   1371 CGTGCTGGTGAATCATCGGAAGAAATCATACAGGGATTCCGGAGAAGAGAAAATTCTCAAGGAA 1430
```

```
Qy    164  LeuTyrMetAlaThrLeuTyrThrTyrThrAsnValAspGluPheGlyAlaSer 183
           |||||              |||||||||||||||||||||||||||||
Db    738  TTCTACATGACTACGTTGTACTACTACAAGACTTACCGGTTGACTTACGGGCGGGCTAAG 797

Qy    184  PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLysArgAlaLeu 203
           ||||||       ||::::||::||||||||||::||::|||||||
Db    798  TTCTTCAACAAGCTTGCTTTCACAACTCGCCCTGTTCGGTTGGGGATCCCAGAAGCGGTTG 857

Qy    204  LysGlnIleIleLeuArgSerAsnLeuProLeuAspIleGlyTyrThrGluHisSerArg 223
           |||||||||           :||||||||::||            ::
Db    858  AAGGCGTTGGTTAGAGACAACCTTCCCGTTGACCGTTGGAACC---CACCCTGAGGCCACC 914

Qy    224  LeuGlnHisIleThrSerSerTyrLysAspThrTyrMetAspThrGlnIleProAlaLeuPro 243
           |||||||||||||||||||:::||                |||||||||||||
Db    915  ATCCGGCAAATAGCTACGCCGAGTACACATGAACCAGGTGCCTCGCCGATGACC 974

Qy    244  LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly 263
           ||||||||               ::||||||||||||::::
Db    975  TCGTTCGCTCGGGCGTTTCTCCAAGATGGCTACTAAGACTCTTGTTGGTTACCGTCACGGAC 1034

Qy    264  TyrValAspThrProTrpTyrLysLysTrpTyrMetLysLeuLysAsnPheMetValAsn 283
           ||||||||||||           ||||||||||
Db   1035  TACGTCGATTTGCCCGCCGTACAAGAAGGTGGTACTACTACAAGACTCATTGTGAAC 1094

Qy    284  ArgValPheIleProThrLysLysPhePheAsnLysLeuGluIleArgGluProSerLys 302
           |||       :::                   |||
Db   1095  ---TTCTTTACTGACCCTGCCAAGTTGATTATGAAGCACACGTCTCTCAGCCCTGTAAAGACT 1151

Qy    303  AlaLeuLysGluLysValSerThrArgAspThrLysAspLeuPheGluAsnLysIleGlyGln 322
           |||                 ::||||||||||       |||       ::||
Db   1152  GCCTACACAAAGCTGGTCCCGAAGCACGCATCCAGAGAAATGTCGTCGGTCAA 1211

Qy    323  GlyThrValAspPhePheAsnLysGluIleArgAspProSerLysLysAlaLeuLysGluLys 342
           |||||||||           :::         |||||||||
Db   1212  AGCACCAAGACAATATTGCCAAC---GGTGTACGTGATTTGTCAAGGATGAATTAAGGAG--- 1265

Qy    343  ValSerAsnAspAlaLysAspLeuPheGluAsnLysIle------------Gly 356
           :::::                                     ||
Db   1266  ------------CCTAGCCAACAAATAATTCGTGAAGAAGCTGCCTCACTACCTTTCTAAGGCA 1316

Qy    357  GlnGlyThrValAspPheIleAsnAsnGluIleArgAsp-----ProSerLysAlaLeu 374
           ::||||||||||                 |||           |||
Db   1317  AAGGGAGACCGTTGACCACGTTGTTAAGAACGTTAAATCCGTTGTGCCGATAAAG----- 1370

Qy    375  IleArgLysValSerThrGlyAlaGluAspLeuAsnGluIleGlyGlnGlyThr 394
           |||||||||||              :::
Db   1371  ---CAAAAGGGCGACCAACCATCCGAAGCAACGCTGTAGGAGAAACCGTTCCGTCTGCC 1424

Qy    395  ValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuLeuIleArgLysValTyr 414
           |||                    :::
Db   1425  ---GATTCCCGCGGAAACTGAATTTGAGGTCCCTGAGAACAAATACGTGACGTGTTACT 1481

Qy    415  Thr------------GluAlaAspAsp 419
           |||            :::||||||||||
Db   1482  ACTCAGGAGGTTAACAGCGAGAGAAGGTTGATGCCGACGAT 1520
```

US-09-807-459-2 (1-458) x BBODNAB (1-2005)

```
Alignment Scores:
Pred. No.:
Score:              790.00
Percent Similarity: 60.34%      Matches:      170
Best Local Similarity: 41.36%   Conservative:  78
Query Match:           33.49%   Mismatches:   133
                                Indels:        30
                                Gaps:          10
```

```
Qy      4  SerAspSerValGlyAspValThrLysThrLeuLeuLeuAlaAlaSerGluSerValAspSer 23
           :::          ::||||||||||||||||||||||||||||            ||||
Db    282  GCAGAGGTGTGGTTGGATGTGTCCAAGACCTTGCTGCAGCCAACGAGGTTGTCAAATCCT 341

Qy     24  AlaAlaAsnAlaThrTyrMetIleAsnAsnSerAspMetSerAspTyrLeuSerAlaValAlaValAspAsp 43
           |||            ::||||||                     :::
Db    342  GAAATGGAAGCAGCTTCAGATTAACGAAGAGATATAGAAGAATTCAGTTGGGAACGTCAAGGAG 401

Qy     44  AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAlaSerVal 63
           |||       |||                 ||||||::||
Db    402  ACCATGCGTTGATGAGGTCTCCAGAAAAAGATGCTGGAAGCCCTAGGTGCCGCAAGAGCGTA 461

Qy     64  SerAlaTyrMetSerArgCysAlaLysGlnAsnAspCysSerLeuThrLeuGlnSerLeuLysTyr 83
           |||||||||           :::         |||||||||
Db    462  AATTGCCTATAGTTGACCGTTGTGATGAGGGCGAGTTGTCTGACGCGTTGACAGCATG----- 515

Qy     84  ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla 103
           |||                 :::::
Db    516  ------------AAGTACAAGCCGTTGACTCTGCCAAATCCTTACCAGTTGGAGGCTGCC 563

Qy    104  PheIleLeuPheLysGluLeuSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp 123
           |||::||||||||||||::||||||||::||||||                 |||
Db    564  TTCATCCTTTTCAAGGAAAGTGATTCTAACCCTGCCAATAGTACCGAAGAGAAAAGTGTTCTGG 623

Qy    124  MetArgPheArgArgGlyLysAsnHisSerThrTyrPheHisAspLeuValPheAsnLeuLeu 143
           ||||||                 :::
Db    624  ATGCGGTTCGAGG----------AGCACGCCACGGCGACTACCATCACACTTTGTTGTTGTTG 677

Qy    144  GluLysAsnValThrArgAspAlaLeuAspAlaThrAspAspIleGluAsnPheAlaSerArgTyr 163
           |||::||||||||||||||||::||||||||||                 :::
Db    678  AAGAAGAATGTTGTACCGCGAGACCCTGAATCCAATCAAATCGAACTTCCCATCCCAGTAC 737

Qy    164  LeuTyrMetAlaThrLeuTyrThrTyrThrAsnValAspGluPheGlyAlaSer 183
           |||||              |||||||||||||||||||||||
Db    738  TTCTACATGACTACGTTGTACTACTACAAGACTTACCGGTTGACTTACGGGCGGGCTAAG 797

Qy    184  PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLysArgAlaLeu 203
           ||||||       ||::::||::||||||||||::||::|||||||
Db    798  TTCTTCAACAAGCTTGCTTTCACAACTCGCCCTGTTCGGTTGGGGATCCCAGAAGCGGTTG 857

Qy    204  LysGlnIleIleLeuArgSerAsnLeuProLeuAspIleGlyTyrThrGluHisSerArg 223
           |||||||||           :||||||||::||            ::
Db    858  AAGGCGTTGGTTAGAGACAACCTTCCCGTTGACCGTTGGAACC---CACCCTGAGGCCACC 914

Qy    224  LeuGlnHisIleThrSerSerTyrLysAspThrTyrMetAspThrGlnIleProAlaLeuPro 243
           |||||||||||||||||||:::||                |||||||||||||
Db    915  ATCCGGCAAATAGCTACGCCGAGTACACATGAACCAGGTGCCTCGCCGATGACC 974

Qy    244  LysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGly 263
           ||||||||               ::||||||||||||::::
Db    975  TCGTTCGCTCGGGCGTTTCTCCAAGATGGCTACTAAGACTCTTGTTGGTTACCGTCACGGAC 1034

Qy    264  TyrValAspThrProTrpTyrLysLysTrpTyrMetLysLeuLysAsnPheMetValAsn 283
           ||||||||||||           ||||||||||
Db   1035  TACGTCGATTTGCCCGCCGTACAAGAAGGTGGTACTACTACAAGACTCATTGTGAAC 1094
```

```
RESULT 22
LOCUS       A16434                  1371 bp    DNA     linear   PAT 23-MAR-1994
DEFINITION  A16434 (lambda GEM-11 #9) gene 2 encoding a 21IB4/rhoptry protein
            homologue.
ACCESSION   A16434
VERSION     A16434.1  GI:511983
KEYWORDS    .
SOURCE      Babesia canis.
  ORGANISM  Babesia canis
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 1371)
  AUTHORS   Babesia.
  TITLE     BABESIAL ANTIGENS
  JOURNAL   Patent: WO 9314204-A 13 22-JUL-1993;
FEATURES             Location/Qualifiers
     source          1..1371
                     /organism="Babesia canis"
                     /db_xref="taxon:5867"
     gene            1..1371
                     /gene="21IB4/rhoptry protein homologue"
     CDS             1..1371
                     /gene="21IB4/rhoptry protein homologue"
                     /codon_start=1
                     /protein_id="CAA01285.1"
                     /db_xref="GI:511984"
                     /translation="MRLVKQAIGTLVLAPTSAPAYKVPGFGGILSKSDGAEKTLSTL
                     NVDASTRAALEGYRMNAAMANPSNGRREEEEAVCGNIAEETECQKSVAEYVESCVR
                     YDCFSIENQKYPQEKEYQPLTLENPYQLEAAFVFVRNSESNPIKNPTEAFWMRPHGG
                     RYGAYHNFLVNILYKNLSDSMVDDNLEGFVRVKAYMATMYYKTTALDVVNARIINKI
                     AFSRHLFGRQIRNALTNIIRSNIPEDFGKYNVDRLRHVMGGYEEYMMKQVPSLPENFAK
                     KYAGMVVKSLIKNVGAYQKQPWFKKLNNQIRNFFVNKIHEPTKEFFVNKIHEPTKEFF
                     VNKIHEPTKEFFVNKLHEPTKEFFSNMVPGAFQK
                     ISEKAGRHLRSSKTVVPEDEPSSSLENEAVEDGQLTMGDVTDFEMATPTYEQSSQESL
                     NEVGNE"
ORIGIN
BASE COUNT        418 a       312 c      325 g      316 t
```

```
Alignment Scores:
Pred. No.:           1.84e-53
Score:              770.50            Length:             1371
Percent Similarity:  55.65%           Matches:            161
                                      Conservative:        95
```

```
US-09-807-459-2 (1-458) x A16434 (1-1371)

                                 Best Local Similarity:  35.00%
Query Match:                     Matches:     161    Mismatches:   161
DB:                                   6            Indels:       43
                                  32.66%              Gaps:          9
```

```
Qy    1  MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer   20
            :::    ||||||:      ::|  |||        ||  |||||||
Db    1  CTTTCTAAATCAGATAGGAGCCGAAAAAGACCTTCTACCTTTCTTAACGTTGACCCATCG   20

Qy   21  ValAlaSerAlaAlaAsnAlaThrMetIleAsnSerAsnSerAspThrTyrLeuSerAla   40
            ||        ||   |||           |||       |:   :|||::||| ||
Db   91  ACGAGACGCGGCTTTAGAAGGCGTTTACACAGAATGAATGCTGCTAAAACTTTTCAAACGGT  150

Qy   41  ValSerAspAsnPheAlaLysGluArgIleCysSerSerGlnValProLysGlySerAsnCysSer   60
               ::|       |||         ::    |||    |||  ||| |  :::  |||
Db  151  ACGAGACGCGGCTTTAGAAGGCGTTTACACAGAATGAATGCTGCTAAAACTTTTCAAACGGT  210

Qy   61  AlaSerValSerAlaThrTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuSer   80
            |||      |||         || |  :  ||       |  :|  |||||::|||
Db  271  AAGAGACGCTAGCGTGAGCGTATGTTGGAAAAGCTGGATGTCGGAAGGTTAGGACATCAG  330

Qy   81  LeuLysThrTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeu  100
            ||||||::||| ||     |||     ||:  ||| ||| |||  |||| |||||
Db   81  CAGAAGTACCCTCAAGGACAAGAATGAATACCAGGCCGCTACACCCTTATCAAATTG  390

Qy  101  GluAlaAlaAlaPheIleLeuPheLysGluSerAspAlaAlaAsnProAlaAsnSerThrGlyLys  120
         ::||||:        |||         |||   |||  |||:    ||| ::  |||  :::|||
Db  331  CAGAAGTACCCTCAAGGACAAGAATGAATACCAGGCCGCTACACCCTTATCAAATTG  390

Qy  121  ArgPheTrpPheMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe  140
            ||||||||||||||||||||||||||      ||||::   :      |:      ::|:
Db  571  CGCAAATAATGCTTACAATGGGCACCAATAAGAACATTACAACCCTTTGGAATGGTGTA  630

Qy  141  AsnLeuLeuGlyLysAsnGlnValThrArgSerAsnLeuProLeuAspPheIleGlyThrGlnHisSer  160
         |||||||||||||||||||||:::||    :|| |||       :|:::    |||  |||
Db  451  GCTTTCTGGATCGGTTTCGTCACGCGGGACGCTTATGCGGCCTATACACACTTTCCTGGTG  510

Qy  161  SerArgTyrLeuThrTyrMetAlaThrLeuThrTyrTyrLysThrTyrThrAsnValAspGluPhe  180
            ||||:::||||||||||||||||||||  :||   |||||||       |||:||::
Db  511  AATATTCTATATAAAAAACCTGACGATAGCATAGCGTGATAGAGAGGTTCGTA  570

Qy  181  GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrIleLys  200
            |      ||||  :::||||||       |||  ||| ||||  |:|::::
Db  631  AATGCCAGGATCATTAACAAAATTGCCTTCTCCCGGCCACTTGGTTAATGAACC  690

Qy  201  ArgAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAspIleGlyThrHisSer  220
         |||||||      ||::||||||||:    ||| |||  ||||||   |||
Db  691  AACGCCCTAACGAATATAATCCGCAGTAACATTCCCGAAGACTTCGGC---AAGTACAAC  747

Qy  221  ValSerArgTyrLeuGlnHisIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro  240
            ||||||:::|||||||:        :::|||       |:::::|||::   ::||||
Db  748  GTTGACCGCCTGAGGCACGTGATGGGTGGCTACGGAGAGTACATGATGAAGCAAGTACCA  807

Qy  241  AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr  260
            |  ::|||:|||||||||        |||  :::||  |||  |:  |:::   |||
Db  808  TCTCTCCACAAATTTCCCAGAAAATACGCGGAATGGTGGAAGTTTAATTAAGAAT  867

Qy  261  ValAlaGlyTyrValAspThrProTrpProTyrLysTyrMetLysLysIleAsnPhe  280
         ||||||        ::||||||||||||||||     |||  :||   :|:|:||
Db  868  GTGGGAGCTTACCAGAGAGCACGGCCATGGTTCAAAAGCTGTGACAATAAGAAAACTTC  927

Qy  281  MetValAsnArgValPheIleProThrGlyLysLysPheAsnLysGluIleArgGluPro  300
            ||:::||  |||  |||        :||   ||||||||||||||||||||||
Db  928  TTCGTGAACAAGATCCATGAAACCCACCAAGAGTTCTTCGTGAACAAGATCCATGAACC  987

Qy  301  SerLysAlaLeuLysGluLysValSerThrAspThrLysLeuPheGluAsnLysIle  320
            |||||||||||      ||||||||||||||||||||||||||||||||||
Db  988  ------------------------ACCAAGAGTTCTTCGTGAACAAGATC  1014

Qy  321  GlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLys  340
            ||| ||:::||::||||| |||||||||||||::  ::|||||||:::|||||||||
Db 1015  CATGAACCCACCAAGGAGTTCTTCGTGAACAAGATCCATGAACCCACC------  1062
```

```
RESULT 23
BBORHOPCN
LOCUS       BBORHOPCN    2796 bp    DNA    linear    INV 26-APR-1993
DEFINITION  Babesia canis putative (60.2) rhoptry protein gene, complete cds.
ACCESSION   M91168
VERSION     M91168.1  GI:155908
KEYWORDS    rhoptry protein.
SOURCE      Babesia canis
ORGANISM    Babesia canis (strain Townsville) DNA.
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2796)
AUTHORS     Dalrymple,B.P., Casu,R.E., Peters,J.M., Dimmock,C., Gale,K.R.,
            Bose,R. and Wright,I.G.
TITLE       Characterisation of a family of multi-copy genes encoding rhoptry
            protein homologues in Babesia bovis, Babesia ovis and Babesia canis
JOURNAL     Mol. Biochem. Parasitol. 57, 181-192 (1993)
MEDLINE     93165069
FEATURES             Location/Qualifiers
     source          1..2796
                     /organism="Babesia canis"
                     /strain="Townsville"
                     /db_xref="taxon:5867"
     CDS             1030..2400
                     /note="putative"
                     /codon_start=1
                     /product="rhoptry protein"
                     /protein_id="AAA27807.1"
                     /db_xref="GI:155909"
                     /translation="MRLVKQAIGTLVLAFTTSAFAYKVPGPGGILSKSDGAEKTLSTL
                     LNVDASTRRALEGYRMNANMANFNSNGREEEEEAVCGNIAEETECQKSVAREYVESCVR
                     YDCFSIENQXYPQEKKYQPLTLPNPYQLEAAFYVFRNSESNPIKNPTEAFWMRFRIGG
                     RYGAYHNFLVNILYKNLSDSMVDDNLEGYVRKYAYAMATMIYKTYTALDVVNARIINKI
                     AFSRHLFGRQIRNALTNIIRSNIPEDFGKYNVDRLRHVMGGYEEYMMKQVPSLPNFAK
                     KYAGMVVKSLIKNVGAYQOKQPWFKKLNNQIRNFFVNKIHEPTKEFFVNKIHEPTKEFF
                     VNKIHEPTKEFFVNKIHEPTKEFFVNKLHEPTKEFFSNMVPGAFQK
                     ISEKAGRHLRSSKTVVPEDEPSSSLENEAVEDGQLTMGDVTDFEMATPTYEQGSQESL
                     NEVGNE"
     repeat_region   1966..2181
                     /rpt_unit=1966..2001
BASE COUNT    872 a    570 c    580 g    774 t
ORIGIN
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Alignment Scores:

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Pred. No.:                4.37e-53          Length:         2796
Score:                    770.50            Matches:        161
Percent Similarity:       55.65%            Conservative:   95
Best Local Similarity:    35.00%            Mismatches:     161
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                                      Query Match:   32.66%        Indels:   43
                                      DB:            3              Gaps:     9

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Qy     1  MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer   20
Db  1420  ...

Qy    21  ValAspSerAlaAlaAsnAlaThrTyrMetIleAsnSerAspMetSerAspThrTyrLeuSerAla   40
Db  1480  ...

Qy    41  ValSerAspAsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSer   60
Db  1540  ...

Qy    61  AlaSerValSerAlaThrTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer   80
Db  1600  ...

Qy    81  LeuLysThrTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProThrTyrGlnLeu   100
Db  1660  ...

Qy   101  GluAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys   120
Db  1720  ...

Qy   121  ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrrProHisHisAspLeuValPhe   140
Db  1777  ...

Qy   141  AsnLeuLeuGluLysAspSerValThrArgAspAlaAspAlaThrAsphrAspIleGluAsnPheAla   160
Db  1837  ...

Qy   161  SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPhe   180
Db  1897  ...

Qy   181  GlyAlaSerPhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGlyIleLys   200
Db  1957  ...

Qy   201  ArgAlaLeuLysGlnIleIleIleGluArgSerAsnLeuProLeuAspIleGlyThrGluHisSer   220
Db  2017  ...

Qy   221  ValSerArgLeuGlnHisIleIleThrSerSerTyrLysAspTyrMetAspThrGlnIlePro   240
Db  1720  ...

Qy   241  AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnAsnArgLeuAlaThr   260
Db  1777  ...

Qy   261  ValAlaGlyTyrValAspThrProThrPThrrLysLysTrpIleTyrMetLysLysAsnPhe   280
Db  1837  ...

Qy   281  MetValAsnArgValPheIleProThrLysLysPhePheAsnLysLysGluIleLeuArgGluPro   300
Db  1897  ...

Qy   301  SerLysLysValSerLeuLeuLysSerValSerThrAspThrLysAspLeuPheGluAsnLysIle   320
Db  1957  ...

Qy   321  GlyGlnGlyThrValAspPhePheAsnLysGluIleArgAspProSerLysAspLeuLysLys   340
Db  2044  ...
```

```
RESULT 24
A16432
LOCUS        A16432         1491 bp    DNA    linear    PAT  23-MAR-1994
DEFINITION   (Lambda EMBL3 #5) gene 5 encoding 21B4/rhoptry homologue.
ACCESSION    A16432
VERSION      A16432.1  GI:511981
KEYWORDS     .
SOURCE       Babesia ovis.
  ORGANISM   Babesia ovis
             Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
             Babesia.
REFERENCE    1  (bases 1 to 1491)
  AUTHORS    .
  TITLE      BABESIAL ANTIGENS
  JOURNAL    Patent: WO 9314204-A 11 22-JUL-1993;
FEATURES             Location/Qualifiers
     source          1..1491
                     /organism="Babesia ovis"
                     /db_xref="taxon:5869"
     gene            1..1491
                     /gene="21B4/rhoptry homologue"
     CDS             1..1491
                     /gene="21B4/rhoptry homologue"
                     /codon_start=1
                     /protein_id="CAA01284.1"
                     /db_xref="GI:511982"
                     /translation="MRAISSVVGCAFWLVAGSTYAIRHQQQANLAPAEVVGDLTHTL
                     KIADEIINAENIHEINRDMHLRLVEEGSSKFIDQICQEVAEDSKCREQVESSYKRCEE
                     NCLQIDEVAYPLNQEYQPLLLPEPYQLDAAFLFKNCESNPARNGLKGPWMRYKEGK
                     EHGDYHHFIISLLGKSLVRKDGVTDLEPLVNKLLYMATYKYKIVIVKKFGARFNTF
                     SFTMNIFGIGIKRALKGIVRSNVPEDMGEHSIERISHLSEGYKDYMLIQVPTLSKFAE
                     RYSDMVMVLLSSLAGYVKAPWYKRWINRFKSLLTGEAYNPDEDIHLLKPIFVDTPRN
                     YIKDALKPLRDAVEENIVNPVDSYLRRKQNISRSQNYNDGHHKIDPSLYEPKRPHIGI
                     AANHARDYIDDKVNKAKELVSAKDRATGIYADHVKPALSDINVVKNDLLDAVNIRN
                     ILRGSSQDDNEQEKTEEKVEEVKPELKQKEVADQPTYVENVKPL"
BASE COUNT      479 a    286 c    328 g    398 t
ORIGIN
```

Alignment Scores:
```
Pred. No.:         1.58e-52
Score:             759.50          Length:           1491
Percent Similarity: 54.04%         Matches:          161
Best Local Similarity: 34.26%      Conservative:     93
Query Match:       32.20%          Mismatches:       173
DB:                6               Indels:           43
                                   Gaps:             8
```

US-09-807-459-2 (1-458) x A16432 (1-1491)

```
Qy      1 MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSer 20
```

```
Db  1168 ATCGGAATTCGTGCGAATCACGCTAGGATATATATAGATAGTGAAGGTAAATAAA------ 1221
         :::|||                                          |||
Qy  360  ValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgGlyValSer  379
Db  1222 ------GCCGAAAGAATTAGTGTCCGCTGCCAAG 1248
Qy  380  ThrGlyAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsn  399
Db  1249 GACCGCGCAACAGGCATATGCAGATCACGTGAAACCTGCTCTGACTGATTACGAAC 1308
Qy  400  AsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyr------ 414
Db  1309 GTTGTAAAGAATTGATCTTCTTGATGCAGTAAAC------ 1362
Qy  415  ---ThrGluAlaAspLeuPheGluAsnLysIleGlyIleGlyGlnGlyThrValAspPheIle 433
Db  1363 AGCTCTCAAAGATGACAATAATCAGACAGAGAGACTGAGGAGAGAAAGTGAGGAAGTT 1422
Qy  434  AsnLysGluIleArgAspProSerLysAlaLeuIleArgLysValTyr 443
Db  1423 AAACCTGAGCTGAAGCAAAAAAGAGTATGCT 1452
```

FEATURES   Location/Qualifiers
     source   1..4145
                     /organism="Babesia ovis"
                     /strain="Ankara"
                     /db_xref="taxon:5869"
     CDS   1..822
                     /partial
                     /codon_start=1
                     /note="putative (60.4)"
                     /product="rhoptry protein"
                     /protein_id="AAA27804.1"
                     /db_xref="GI:155901"
                     /translation="LIYMATTYKTYLIVNNSDAKFFNRIAFATKIFGFGIKKALKDI
                     VRSNVPEYMGEHSIRISHLAHGYKDYMLTQVPTLSKFAERYSDMVMKVLLSSLAGYV
                     KAPWYKRWFNKVKDFPVNKIGKPTKEHFHKKHPRTAEFFDKMHERIKDFFENKIGAPT
                     KDFFENKIGAPTKDFFENKIGAPTKDFFENKLPEHTKDFFENKIGA
                     PIKESPENLGHKRPVNWRYISSPQRMNNDSVADVAVETVDMENHDGGNTVGEMFV"
     CDS   2132..3622
                     /codon_start=1
                     /note="putative (60.5)"
                     /product="rhoptry protein"
                     /protein_id="AAA27805.1"
                     /db_xref="GI:155902"
                     /translation="MRAISSVVGCAFWLVAGSTYAIRHQQQAANLAPAEVVGDLTHTL
                     KIADEIINAENIEHEINRDMHLRLVEEGSKFIDQICQEVAEDSKCREQVESVKRCEE
                     NNCLQIDEVAYPLNQEYQPLLLPEPYQLDDAAFTLFKNCESNPAKNGLKGPWMRYKEGK
                     EHGDVHHFIISLLGKSLVRKDGVTDLEFFLVNKLLYMATTYKTYLLIVKKFGARFNTF
                     SFTMNFIGIGIKRALKGIVRSNVPEDMGEHSIERISHLSEGYKDYMLTQVPTLSKFAE
                     RYSDMVMKVLLSSLAGYVKAPWYKRWINRFKSLLGEAYNEDEDIHLLKFIVDTPRN
                     YIKDALKPRDAVEENIVNPVSDYLRRKONISRSQNYNDGHHKIDPSLYEPKRPHICI
                     AANHARDYIDDKVNKAKELVSAAKDRATGIYADHVKPALSDITNVVNDLLDAVNIRN
                     ILRGSSODDNNEQEKTEEKVEEVVRPELKQKEYADQPTYVENVKPL"

BASE COUNT   1341 a   813 c   846 g   1145 t
ORIGIN

US-09-807-459-2 (1-458) x BBORHOP2OV (1-4145)

```
Qy  1    MetAlaProSerAspSerValGlyAspValThrLysThrLeuLeuAlaLeuAlaSerGluSer 20
Db  2342 GAGGGAAGTAAAATTTATTGATCAAAATTTGTCAGGAAGTCCGCTGAGGAGGATTCTTAAGTGCCGT 2401
Qy  21   ValAspSerAlaLeuAlaAsnAlaTyrMetIleAsnSerAspMetSerSerAspTyrLeuSerAla 40
Db  2402 GAACAAGAGTTGAATACATATGTTAAGCCGGTTCTGAAGAGAACAAACTGTTTACAGATTGACGAA 2461
Qy  41   ValSerAspAsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSer 60
Db  2462 GTAGCTTACCCTTTGAATCAGGAATATCAGCCACTATTACTTCCGGAACAACCATACCAAATTG 2521
Qy  61   AlaSerValSerAlaLaTyrMetSerArgCysAlaLalysGlnAspCysLeuThrLeuGlnSer 80
Db  2522 GATGCTGCCTTCACATTGTTCAAGAACTGTGAGTCTAATCCTGCTAAAAATGGCCTGAAA 2581
Qy  81   LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuLeu 100
Db  2582 GGTCCATGAGATGCGTTACAAGGAGAGGGTAAAGAGACAATGGGA---GAGCACAGT 2641
Qy  101  GluAlaLalaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGlyLys 120
Db  2642 AGTTTGCTCCGGCAAGAGTTGGTTCGTAAGGATGGTGTTACTGACCTTGAGTTCCTCGTC 2701
Qy  121  ArgPheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
Db  2702 AACAAGCTTTTGTACAATGGCCAACCACTACAAAAACCTACCTAATTGTCAAGAAGTTC 2761
Qy  141  AsnLeuLeuGluLysAsnValThrArgArgAspAlaAspAlaThrArgAspIleAsnPheAla 160
Db  2762 GGTCGTCTCGGTTTTCAACACTTACTCTCTGACATGGTTATGAAAGTTCTGTTGAGCGAGTTC 2821
Qy  161  SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrArgAspIleAsnPheAla 180
Db  2822 AGGGCCATTAAAAGGCCATCGTCCGCTCCAAATGTTCCGGAAGCACAGT---GAGCACAGT 2878
Qy  181  GlyAlaSerPhePheAsnLysSerPheThrThrThrGlyLeuPheGlyIleLeuLys 200
Db  2879 ATTGAACGTATTAGTCCATTTGTCCGAAGGATCACAAGGACTACATGTTGACACAGGTGCCA 2938
Qy  201  ArgGlnAlaLeuLysLysGlnIleIleAlaArgSerAsnLeuProLeuAspSerIleGlyLysHisSer 220
Db  2939 ACCCTTTCAAAGTTTGCCGAACGTTACTCTCTGACATGGTTATGAAAGTTCTGTTGAGCGAGC 2998
Qy  221  ValSerArgArgLeuGlnHisIleThrSerSerTyrIleLysAspThrGlnIlePro 240
Db  2999 CTCGCCGCGGTTATGTCAAGGCCTCCAAATGTACAAGAGAATGCAATAGATTTCCTTG 3058
Qy  241  AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr 260
Qy  261  ValAlaLysGlyValAlaPheTrpLeuValAlaGlySerThrTyrAlaIleArgHisGlnGlnGlnAlaAlaAsnLeuAlaProAlaGluValVal 280
Qy  281  MetValAsnArg------ 287
Db  3059 TTAACTGGTGCAAGCTTACAACCCTCATGAGAGATAACATTTACTTAAAACCTATTTCGTT 3118
Qy      ValPheIle 287
```

```
Qy    288  ProThrLysPhePheAsnLysGluIleArgGluProSerLys---AlaLeuLysGlu  306
           |||   :::              |||||::::::|||
Db    3119 GATACTCCTAGGAATTACATAAAAGATGCAACTTAAGCCACTGCGTGATGCTGTAGAGGAA  3178

Qy    307  LysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp  326
                                                 |||
Db    3179 AATATCGTTAACCCGTCAGTGATTATCTCCGACCGCAAGCAAAATATTCTTAGGTCACAA  3238

Qy    327  PhePheAsn------------------LysGluIleArgGluProSerLysAlaLeu  339
                                       ::::|||
Db    3239 AACTACAATGACGGCATCATTAAAAATAGATCCCTCCTTTTATGAACCTAAGACGCGCAT  3298

Qy    340  LysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyGlnGlyThr  359
           :::||| |||::|||   ||||::::|||
Db    3299 ATCGGAATTCCTGCGAATCACGCTAGGATTATTATAGATGATAAGGTAAATAA------  3352

Qy    360  ValAspPheIleAsnAsnGluIleArgGluProSerLysLysAlaLeuArgLysValSer  379
                          |||
Db    3353 ------------------GGCAAAGAATTACTGCTTCCGCTGCCAAG  3379

Qy    380  ThrGlyAlaGluAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIleAsn  399
           ||||| |||::||   ||||::||||
Db    3380 GACCCGCACACAGGCATATATATGCAGATCACGTGAAACCTGCTCTGAGTGATAATTACGAAC  3439

Qy    400  ------AsnGluIleArgGluProSerLysAlaLeuIleLeuArgLysValThr---  414
                 :::||   ::|||
Db    3440 GTTGTAAAGAATGATCTTCTTGATGCCAGTAAAC------ATCAGGAATATATTACGTGGC  3493

Qy    415  ---ThrGlyAlaAspLeuPheGluAsnLysIleGlyIleGlyThrValAspPheIle  433
              ::::: |||::|||   ||||
Db    3494 AGCTTCAAGATGACAATAATGAACAAGACTGAGGAGGAGAAAGTTGAGGAAGTT  3553

Qy    434  AsnLysGluIleArgGluProSerLysAspProSerLysAla  443
           |||::||
Db    3554 AAACCTGACGTGAACGACAAAAAGAGTATGCT  3583
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RESULT 26

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LOCUS       BBORA1P      2549 bp    DNA    linear   INV 09-APR-1996
DEFINITION  Babesia bovis (clone 4-1) rhoptry associated protein 1 (RAP-1) gene
            1, 3' end of cds, rhoptry associated protein 1 (RAP-1) gene 2,
            complete cds.
ACCESSION   L77326
VERSION     L77326.1  GI:1256656
KEYWORDS    rhoptry associated protein 1.
SOURCE      Babesia bovis
  ORGANISM  Babesia bovis (strain Mo7) (clone: 4-1) DNA.
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2549)
  AUTHORS   Suarez,C.E., Palmer,G.H., Hines,S.A. and McElwain,T.F.
  TITLE     The Babesia bovis rhoptry associated protein-1 intergenic region
            encodes a functional eukaryotic promoter
  JOURNAL   Unpublished (1996)
FEATURES             Location/Qualifiers
     source          1..2549
                     /organism="Babesia bovis"
                     /strain="Mo7"
                     /db_xref="taxon:5865"
                     /clone="4-1"
                     /cell_type="merozoite"
     gene            1..2549
                     /gene="RAP-1"
     CDS             <1..1339
                     /gene="RAP-1"
                     /note="gene 1"
                     /codon_start=2
                     /product="rhoptry associated protein 1"
                     /protein_id="AAA96414.1"
                     /db_xref="GI:1256657"
                     /translation="PLSLPNPYQLDDAAFRLFKESASNPAKNSVKREWLRFRNGANHGD
                     YHFPVTGLLNNNVVHEEGTTDVEYLVNNVKVLVLYMATMNYKTYLTVNSMNAKFFNRESFTT
                     KIFSRRIRQTLSDIIRWNVPEDFEERSIERITQLISSYEDYMLTQIPTLSKFARRYAD
     3'UTR           1337..1501
                     /gene="RAP-1"
                     /note="gene 1"
     misc_feature    1501..2377
                     /gene="RAP-1"
                     /note="rap-1 intergenomic region; putative"
     5'UTR           2377..2519
                     /gene="RAP-1"
                     /note="gene 2"
     gene            2519..2549
                     /gene="RAP-1"
     CDS             2520..2549
                     /gene="RAP-1"
                     /note="gene 2; putative"
                     /product="rhoptry associated protein 1"
                     /protein_id="AAA96415.1"
                     /db_xref="GI:1256658"
                     /translation="MRIISGVVG"
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BASE COUNT      848 a    494 c    463 g    744 t
ORIGIN
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                     EPTKKFEMQDTHBKTKGYLKENVAEPTKTFFFKEAPQVTKHFEDENIGQPTKEFFREAPQ
                     ATKHFLDENICQOPTKEFFREAPQATKHFLGENIAQPTKEFFKDVPQVTKKVTTENIAQ
                     PTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTQAKNFISAAHEGTKQFLNETVCGP
                     TKEFLNGALETTKDALHHLGKSSEEANLYDATENTQANDSTTSNGEDTACYL"
```

us-09-807-459-2 (1-458) x BBORA1P (1-2549)

Alignment Scores:

```
Pred. No.:              1.21e-44          Length:         2549
Score:                  565.50            Matches:         146
Percent Similarity:     51.09%            Conservative:     64
Percent Identity:       35.52%            Mismatches:      152
Best Local Similarity:  28.21%            Indels:           49
Query Match:            3                 Gaps:              6
DB:
```

```
Qy    91   ProLeuThrLeuProAspProTyrGlnLeuGluAlaAlaAlaPheIleLeuPheLysGluSer  110
           |||||||
Db    2    CCTCTATCTCTTCCAAACCCTTACCAGTTGGAAGCTGCGTTCAGATTGTTCAAAGAGAGT  61

Qy    111  AspAlaAsnProAlaAsnSerThrGluLysArgPheTrpMetArgPheAsnArgGlyAlaLys  130
           :::::||||||||||      |||||   :::::||||
Db    62   GCATCGAACCCTGCCAAGAACAGCGTAAAACCCGAATGGTTGCGTTCAGAAATGGAGCG  121

Qy    131  AsnHisSerTyrPheHisAspLeuValPheAsnLeuGluLysAsnValThrArgAsp  150
           ||||||           |||   :::
Db    122  AACCATGGTGATTACCACTACTTCGTCGTTGTTGACAACAATGTTGCACAG  181

Qy    151  AlaAspAlaThrAspLeuAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyr  170
           |||||||||||||||
Db    182  GAAGGACTACCGATGTTGAATATCTTGTCACAAGGTACTCTATATGGCTACCATGAAC  241

Qy    171  TyrLysThrTyrThrAsnValAspGluPheGlyValAlaSerPheAsnLysLeuSerPhe  190
           |||||||||||||||||     ||||||||||||
Db    242  TACAAGACTTATTTGACAGTAAACAGTATGAACGCCAAGTTCTTCAACAGATTCAGCTTC  301

Qy    191  ThrThrArgGlyLeuPheGlyTrpGlyIleLeuArgArgAlaLeuLysGlyIleLeuIleArgSerAsn  210
           |||||||      ::::||||
Db    302  ACTACAAAGAATATTCAGTCGCTGTAGGCAAACATTGAGTGATATCATCAGGTGGAAT  361

Qy    211  LeuProLeuAspIleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSerSer  230
           ||||||   :::||||||||||
Db    362  GTTCCTGAAGATTTT----GAAGAAAGGAGCATCGAACGTAACGTTACACTTAGCAGC  418

Qy    231  TyrLysAspTyrMetAspThrGlnIleProAlaLeuProLysPheGluAlaLysPheSer  250
           |||||::|||||||||||||||
Db    419  TACGGAAGATTACATGTTGACCAGATTCCACTCCTTTCCAAAGTTTGCAGCTAAGTTCT  478

Qy    251  LeuMetValValGlnArgLeuLeuAlaThrValAlaGlyTyrValAspThrProTyr  270
           ||||||   :::      ||||||||||||
Db    479  GACATGGTGAAGAAGGTTTCGCTCGGTACGGTTGAAGCTCCTGGTAC  538

Qy    271  LysLysTrpTyrMetLysLeuLysAsnPheMetValAsnArgValPheIleProThrLys  290
           |||        ||||||::::|||
```

```
Db   539 AAAAGATGGATAAAGAAATTCAGAGATTTTTTCTCTAAAAACGTTACCCAACCTACAAAG 598

Qy   291 LysPhe------------------------------------------------ 292
         |||
Db   599 AGTTCAATCGAGGATACTAACGAAGTTACCAAAAAACTATCTGAAAAGCCAAATGTTGCTGAG 658

Qy   293 ----------------------------------------PheAsnLysGlu 296
                                                   :::
Db   659 CCCACTAAAAAGTTTATGCAGGACACTCACGAAAAAGCTATCTGAAAAGAAT 718

Qy   317 IleArgGluProSerLysAlaLeuLysGluLysValSerValPhe 316
         |||::||::::::|||
Db   719 GTAGCCGAAACCTACTAAGACTTTTTTCAAGGAGGCTCCTCAAGTCACCAAAACACTTCTTC 778

Qy   337 LysAlaLeuGluLysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGly 356
         |||::
Db   839 CATTTCCTAGACGAAAAACATCGGTCAACCACCAAGGAGTTCTTC---AGGGAGGCTCCT 895

Qy   357 GlnGlyThrValAspPheIleAsnAsnGluIleArgAspthrhrGlyAlaLeuIleArg 376
         |||
Db   896 CAAGCCACTAAGCCACTTCCTAGGCGAGAATATTGCCTCAACCTACTACAAAGAATTTTCAAG 955

Qy   377 LysValSerThrGlyAlaGluAspLeuPheGluAsnLysIleGlyInGlyThrValAsp 396
         :::|||
Db   956 GAGTCCTCAAGTCACCACAAGGAGTTATAACTGAGAACATTGCTCACCAACTAAGGAG 1015

Qy   397 Phe-------------------------------------------- 397
         |||
Db  1016 TTCCTTAGGGAGGTTCCTCATCCTACCACCAAGGAGTTCTTCATGAAAGTCTTGAATGAAAAACATTGCTCAACCT 1075

Qy   426 GlyGlnGlyThrValAspPheIleAsnAsnGluIleArgAspthrhrGlyAlaLeuIleIle 445
         |||
Db  1133 CATGAAGGTACTAAGCACTTCTTAAAACCAAGACATTGTTGGCCAACTACAAAAGGAATTCCTG 1192

Qy   446 Arg---LysValSerThrGluAlaAspAsnLeu 455
         :::
Db  1193 AACGGAGCTTTAGAAACTACTAAAGACGCCATTA 1225
```

RESULT 27

```
BBORHP2340
LOCUS       BBORHP2340          2851 bp    DNA     linear    INV 26-APR-1993
DEFINITION  Babesia ovis putative (60.2 or .3) rhoptry protein gene, 5' end and
            putative (60.3 or .4) rhoptry protein gene, 3' end.
ACCESSION   M91173
VERSION     M91173.1  GI:155917
KEYWORDS    rhoptry protein.
SOURCE      Babesia ovis
  ORGANISM  Babesia ovis (strain Ankara) DNA.
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 2851)
  AUTHORS   Dalrymple,B.P., Casu,R.E., Peters,J.M., Dimmock,C., Gale,K.R.,
            Bose,R. and Wright,I.G.
  TITLE     Characterisation of a family of multi-copy genes encoding rhoptry
            protein homologues in Babesia bovis, Babesia ovis and Babesia canis
  JOURNAL   Mol. Biochem. Parasitol. 57, 181-192 (1993)
  MEDLINE   93165069
FEATURES             Location/Qualifiers
     source          1..2851
                     /organism="Babesia ovis"
                     /strain="Ankara"
                     /db_xref="taxon:5869"
     CDS             1..966
                     /partial
                     /note="putative (60.2 or .3)"
```

```
     CDS             2276..2851
                     /partial
                     /codon_start=1
                     /note="putative (60.3 or .4)"
                     /codon_start=1
                     /product="rhoptry protein"
                     /protein_id="AAA27812.1"
                     /db_xref="GI:155919"
                     /translation="MRAISSVVGCAFWLVAGSTVAIRHQQQAANILAPAEVVGNVAATL
                     STADEIISSHDYDKELINDMRDQMREMGENFVDTVCTKAPEDSNCRQMVALYADRCEM
                     YGCLQIDNVNYPVDEEYQPLSLPNPYQLDAAFTLFKNSASNPAKNGLKGQWMRRNGK
                     KHGDYHRFLGLLAKGVTRKDGATDLEFLVNK"
ORIGIN
BASE COUNT    885 a    606 c    597 g    763 t
```

```
Qy   304 ---LeuLysGluLysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyGln 322
            ::::|||
Db   361 AAAATAGGCAAAACCTACAAAAGGAACACTTCCACAG-----AACACCCACGCACCGCC 414

Qy   284 ArgValPheIleProThrLysLysPheAsnLysGluGluIleArgGluProSerLysAla 303
         :::::|||
Db   301 TATGTCAAGGCTCCATGGTACAAGAGATGGTTCAACAGGTTAAAGAATTCTTTTGTTAAC 360
```

```
us-09-807-459-2 (1-458) x BBORHP2340 (1-2851)

Alignment Scores:
Pred. No.:                        1
Score:                       632.50
Percent Similarity:          63.36%
Best Local Similarity:       46.58%
Query Match:                 26.81%

          Length:        2851
          Matches:        136
          Conservative:    49
          Mismatches:      90
          Indels:          18
          Gaps:             6
          DB:               3
```

```
Qy    362  PheIleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThrGly 381
           |||                    ||:|||:::|||
Db    595  TTCTTCGAGAACAAGATAGGTGCTCCTACCAA------------------------- 627

Qy    382  AlaGluAspLeuPheGluAsnLysIleGlyValGlnGlyThrValAspPheIleAsnAsnGlu 401
           |||||||||||:||::|||::::|
Db    628  -------GACTTCTTTGAGAACAAGATAGGTGCTCCTACCAAGGACTTCTTCGAGAACAAG 681

Qy    402  IleArgAspProSerLysAlaLeuIle---ArgLysValTyrThrGluAlaAspPheLeu 420
           :::          |||                ||::|||
Db    682  CTGCGTGACGCACCAAGGACTTCTTCGAGAACAAGCTGCCTGAACACACCAAGGACTTC 741

Qy    421  PheGluAsnLysIleGlyThrValAspPheIleAsnLysGluIleArgAspPro 440
           |||||||||||:|||:::||||    :::           :::|||    |||
Db    742  TTCGAGAACAAGCTGCCTGAACACACCAAGGACTTCTTTGAGAACAAGATTGGTGCCCC 801

Qy    441  SerLysAlaLeuIleArgLysValSerThrGluAla 452
           |||:::          |||:::|||
Db    802  ATTAAAGA-ATCATTTGAGAACTTGGGACACAAGCG 836
```

```
RESULT 28

BDRHASPR

LOCUS       BDRHASPR          1483 bp    mRNA     linear    INV 03-JUN-1996
DEFINITION  B.divergens mRNA for rhoptry associated protein.
ACCESSION   Z49818
VERSION     Z49818.1  GI:974766
KEYWORDS    rhoptry associated protein.
SOURCE      Babesia divergens
  ORGANISM  Babesia divergens
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 1483)
  AUTHORS   Skuce,P.J., Mallon,T.R. and Taylor,S.M.
  TITLE     Molecular cloning of a putative rhoptry associated protein
            homologue from Babesia divergens
  JOURNAL   Mol. Biochem. Parasitol. 77 (1), 99-102 (1996)
  MEDLINE   96379225
REFERENCE   2  (bases 1 to 1483)
  AUTHORS   Skuce,P.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-1995) Skuce P. J., Department of Agriculture for
            Northern Ireland, Veterinary Sciences Division, Stoney Road,
            Stormont, Belfast, Northern Ireland, BF4 3SD
FEATURES             Location/Qualifiers
     source          1..1483
                     /organism="Babesia divergens"
                     /strain="Drumaness"
                     /db_xref="taxon:32595"
                     /clone_lib="Unizap-XR"
                     /dev_stage="merozoite"
     5'UTR           1..121
     sig_peptide     122..184
     CDS             122..1348
                     /codon_start=1
                     /product="rhoptry associated protein"
                     /protein_id="CAA89970.1"
                     /db_xref="GI:974767"
                     /db_xref="SPTREMBL:Q17129"
                     /translation="MKGFSRIVALCVVATKSTFALRHAAQNGANAVALGEPDSVAEAI
                     ETVDSVMAAIQESVKTMDNMNIAHLSTRSEGFVDDVCQGVNEESCQESRTYVSRCIQ
                     RGCLKIDHERYAAEKGNQPLAFPNPYQVGAFQLFQECDSDPTQGNRFRKHGG
                     RYGAYQSFIMNVVTSSYTQLSDNIEVEDLVNRYLYMATMYKTVLLDTTRKVHLINKI
                     DRGHHISGKSIKHMVEKIIRNHLPRDFGIYSIERLSHISAGYGDYILKQVPYMPAFST
                     RFNRMVVDFLHKIIGKYQKMPWPYKWFNSVADFFKNSIGKPIKNLFSKRAPSSTEGA
                     WHKKVSHSVKKMLNEKIPVVKNFFKDGIRKSSLGDLLHGPKASSMKEDEVPLTEAMET
                     NESSGENLRGYRHGLR"
     mat_peptide     185..1345
                     /product="rhoptry associated protein"
     3'UTR           1349..1483
BASE COUNT       404 a    356 c    350 g    373 t
ORIGIN
Alignment Scores:  .
```

```
Pred. No.:               .
Score:                  3.62e-37          Length:          1483
Percent Similarity:      569.50           Matches:          125
Best Local Similarity:   54.12%           Conservative:      59
Query Match:             36.76%           Mismatches:       137
DB:                      24.14%           Indels:            19
                                          Gaps:               6
```

```
us-09-807-459-2 (1-458) x BDRHASPR (1-1483)

Qy     5  AspSerValGlyAspValThrLysThr--------------------LeuLeuAlaLaSerGluSer 20
          ||||||||:|||::|        :::|||                     ||||||     |||||||
Db    233  GATAGCGTGGGCGTCGACGTAACGAAGCCATTGAACACAGTGCGATTCTGTCAGGAGAATCCAGTGAAAGC 292

Qy    21  ValAspSerAlaAlaLysAsnAlaThrTyrMetIleAsnSerAspMetSerAspTyrLeuSerAla 40
          ||         |||                        |||::|||||||::||||||
Db    293  GTGAAGACTATGGATAAC------------------------ATGATTGCCCATCTGTCTACC 331

Qy    41  ValSerAspAsnPheAlaGluArgIleCysSerSerGlnValProLysGlySerAsnCysSer 60
          :::|||         :::              |||:::              :::|||
Db    332  CGCTCCGAGGGCGTTTGTTGTTGATGATGTTTGCCAGGGTGTCAAGCAGGAGAGTCCCAGTGCCAA 391

Qy    61  AlaSerValSerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSer 80
          ||||||                  ||||||::||||||            |||    ::: |||
Db    392  GAATCCGTGCGCACCTACGTTAGTCGTTGCATAAAGCAGGATTGCCTCAGGATTGACCAC 451

Qy    81  LeuLysTyrProLeuGluAlaLysThrGlnProLeuThrLeuProAspProTyrGlnLeu 100
          |||         |||         :::              |||||||:::::
Db    452  GAGAGATATGCCGCTGAGAAAGAAACAACCGTTAGCCTTTACGGTGCTTACCAGTG 511

Qy   101  GluAlaAlaAlaPheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLys 120
          ||||||||              ::: |||:::              |||:::|||
Db   512  GGCGCTGCTGCTTTCCAATTGTTCAAGGAGTCGGACGCCAACCCAGCAAACTCAACGGC 571

Qy   121  ArgPhePheTrpMetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPhe 140
          |||||         ||||||:::              :::              :::
Db   572  AATTTTGGGATGCGGTTCAAGCAATGGTGGTCGTTCACTACTACCAGAGCTTTATAATG 631

Qy   141  AsnLeuLeuGluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheA 160
          |||:::              :::|||::              |||:::              |||
Db   632  AACGTTGTAACGTTCCAGCTACACTCAGTTGTCTGCAACACCGAAGTGGAGGACTTGGTT 691

Qy   161  SerArgTyrArgLeuTyrMetAlaThrLeuTyrArgTyrTyrThrArgAsnValAspGluPhe 180
          |||         |||              |||                  :::              |||
Db   692  AACAGGTACCTCTACATGGCCACCAGTGTACTAAAGAACGTACCTCATCCTGGACACCACC 751

Qy   181  GlyAlaSerPhePheAsnLysSerPheThrThrArgGlyLeuPheGlyTrpGlyIleLys 200
          |||              |||              |||         |||||||    :::
Db   752  AAGGTTCAATCGAATTAACAAGGATTCCTGGGCATCACAGTCTCCGGCGAAGAGCCATTAAG 811

Qy   201  ArgGlyAlaLeuLysGlnIleIleLeuArgSerAsnLeuProLeuAspProLeuAlaThr 220
          :::||||||              :::              |||         |||
Db   812  CACATGGTTGAGAAGATCATTCGTAACCATCTCCCAGGATTTCGGGCATC---TACAGC 868

Qy   221  ValSerArgTyrLeuGlnHisIleThrSerTyrLysAspTyrMetAspThrThrGlnIlePro 240
          :::              |||         ::: |||                        |||:::              |||:::
Db   869  ATTGAGAGGCTGAGCCACATTACCAGCTACAAGGACTACATGGACACCACCCAGGTTCCG 928

Qy   241  AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgGlyLeuLeuAlaThr 260
          |||:::              |||:::||||||              |||                        |||:::
Db   929  TATATGCCTGCATTCTCTACTCGGCTTCAACAGGATGGTCGTGAGATACCCTCCACAAAGATC 988

Qy   261  ValAlaGlyTyrValAspThrProThrTyrLysLysTrpTyrMetLysLeuLysAsnPhe 280
          |||:::              |||                     |||:::||||||
Db   989  ATCGGTAAATACCAGAGACATGCCGATAGAGAAATGGTTCAACAGTGTTGCAGACTTC 1048

Qy   281  MetValAsnArgValPheIleProThrLysLysProPheAsnLysGluIleArgGluPro 300
          |||:::              :::||||||              |||              |||:::
Db  1049  TTCAAGAACAGCATTGGAAAGCCTATCAAAAACTTGTTCAGCAAG-----CGTGCTCCA 1102

Qy   301  SerLys----------AlaLeuLysGluLysValSerThrAspThrLysAspLeuPhe 316
          |||              |||:::|||||||:::|||
Db  1103  TCTTCTTCTTACTGAGGGGGGCATGGCACAAGAGAAGGTTTCCACTCTGTGAGAGAGATGTTA 1162
```

```
Qy    317  GluAsnLysIleGlyGlnGlyThrValAspPheAsnLysGluIleArgAspProSer  336
            :||||||                              ||||
Db   1163  AACGAGAAGATC---CCTGTGTTGTTAAGAATTTCTTCAAGGAGGCATTAGGAGAGGCTCT  1219
```

RESULT 29

```
LOCUS       AF026272              4414 bp    DNA     linear   INV 03-NOV-1997
DEFINITION  Babesia bigemina RAP-1c (rap-1c) gene, complete cds, and
            YJR070c-like protein (YJR070c-like) gene, partial cds.
ACCESSION   AF026272
VERSION     AF026272.1  GI:2583051
KEYWORDS    .
SOURCE      Babesia bigemina.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1  (bases 1 to 4414)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Genomic cloning of Babesia bigemina rap-1c gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 4414)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-SEP-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES             Location/Qualifiers
     source          1..4414
                     /organism="Babesia bigemina"
                     /strain="Mexico JG-29"
                     /db_xref="taxon:5866"
     misc_feature    1..380
                     /note="rap-1b 3' intergenic region"
     gene            <1027..>2559
                     /gene="rap-1c"
     mRNA            <1027..>2559
                     /gene="rap-1c"
     CDS             1027..2559
                     /gene="rap-1c"
                     /note="similar to Babesia divergens rhoptry associated
                     protein encoded by the sequence presented in GenBank
                     Accession Number Z49818"
                     /codon_start=1
                     /product="RAP-1c"
                     /protein_id="AAB82596.1"
                     /db_xref="GI:2583052"
                     /translation="MIHYACLIIAICALSLRSVAAVRYGGHAMIMAPDHTVEPAVDPV
                     DDTKOLLEDSEQIEKAMQEEIGLINDDSIRAEMCLGSKDEHHCASQIAAYVARCKEGN
                     CLTIDAVGKPQNKAYKQLVLPDYQLHAAFLLFKNCRRNESRHWMDRFWMRFKRGGRY
                     AAYSFSLNLLRRNLPLGDDKNALHGFVOKYFYMTAIYYKTYLSLDAINAKIENKIAL
                     AKHILGPKIKRALRKIVEANKPSALOANDVKAIRPLAYGYRQYMASQIPSLPFAYRF
                     SSMVVTALVDNLTGVRAOQOPWYKRWFGCKVKNLFTGKQPSEKAYEIDEPIATEEETEVE
                     ENKSVFGKVKEKLGINIRFNTGIFRKGEAKTRHSHLSEEDIMGSLSSADALLEPVLDVM
                     DLMHEDEEQPESDELPAKRRKASSTGYKKFFKNILDTGAIKDAASRIGFPKKYFKR
                     SS"
     gene            <3933..>4394
                     /gene="YJR070c-like"
                     /product="YJR070c-like protein"
     mRNA            join(<3933..4144,4204..4309,4350..>4394)
                     /gene="YJR070c-like"
                     /product="YJR070c-like protein"
     CDS             join(<3933..4144,4204..4309,4350..>4394)
                     /gene="YJR070c-like"
                     /note="similar to Saccharomyces cerevisiae ORF YJR070c
                     protein encoded by the sequence presented in GenBank
                     Accession Number Z49570"
                     /codon_start=1
                     /product="YJR070c-like protein"
                     /protein_id="AAB82597.1"
                     /db_xref="GI:2583053"
                     /translation="MADIAAAVEDFSKLEEFSKPDAELLSKILFSPDVKLSLQLRALY
                     FCRDLKSSECATLLKKALDVHYDAFLRHETAYVIGQAGCEEASDVLVKLLEDENEDPM
                     VRHEAEAVAAIGGKRFID"
BASE COUNT     1213 a   1030 c   1087 g   1082 t      2 others
ORIGIN
```

```
Alignment Scores:
Pred. No.:
Score:                    2.02e-35        Length:        4414
Percent Similarity:         555.00        Matches:        147
Best Local Similarity:      44.34%        Conservative:    80
Query Match:                28.71%        Mismatches:     177
DB:                         23.53%        Indels:         108
                                 3        Gaps:            15
```

US-09-807-459-2 (1-458) x AF026272 (1-4414)

```
Qy      1  MetAlaProSer--------------------------AspSerValGlyAspValThrLysThr    13
            |||||||                              |||    ||||||
Db   1117  ATGGCCCCTGACCACACTGTCGAGGCCTGCCGGTTGATCCCGTCGACGACGACAACCAAGCAG  1176

Qy     14  LeuLeuAlaAlaSerGluSerValAspSerAlaAlaAsnAlaAlaTyrMetIleAsnSerAsp    33
            ||||||          ||||||              :::::       |||
Db   1177  CTYCTCGAAGACACGACGACAGAGTTGAGAGAGGCC------------------------     1209

Qy     34  MetSerAspThrLeuSerValAlaValSerAspAsnPheAlaAlaGluArgIleCysSerGlnVal    53
            |||           ||         :::::    :::::             |||
Db   1210  ATGGAGGAGGAAATCGGACTGATCAACGATGACTCCATTCGCGAAATGTGCCTGGGCAGC    1269

Qy     54  ProLysGlySerAsnCysSerAlaSerValSerAlaThrMetSerArgCysAlaLysGln    73
            ::||:||||||:::::|            :::|||||||        :::||||||
Db   1270  AAGGACGAGCACCACCATTGCCCATCCAAATCGCTGCTACGTTGCCCGTTGCCAAGGAAGGC  1329

Qy     74  AspCysLeuThrLeuGlnSerLeuLysTyrProLeuGluAlaLysTyrGlnProLeuThr     93
            ::::||||||||||:::::           :::::   ::::::       ||
Db   1330  AACTGCCTCACCATCGACGCCGTGGGAAAACCCGAACAAAGCACCTACGTC  1389

Qy     94  LeuProAspProTyrGlnLeuGluAlaAlaPheIleLeuPheLysGluSerAspAlaAsn    113
            ||||||          ||||||       ||||||:::::||||||         |||
Db   1390  CTGCCCGACCCCTACCAGTTCCAGGTTCAAGAGGCCAAC------------------     1449

Qy    114  ProAlaAsnSerThrGluLysAspArgPheMetArgPheArgGlyLysAsnHisSer    133
            ::                ||                  ::||
Db   1450  GAGAGCACAGGCCACTGGATGGACAGGTTCTGGATGCGTTTCAAGAGGGGAGGGCGTTACGGT  1509

Qy    134  TyrPheHisAspLeuValPheAsnLeuLeuGlyLysAsnValThrArgAspAlaAspAla    153
            ||||||||        :::::::::::           :::|||
Db   1510  GCTTACTTCAGCTTCAGCCTCAACCTGTTGAGGCGCAACCTGTTCCTCGGCGACGACAAA  1569

Qy    154  ThrAspIleGluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThr    173
            :::||||||      :::|||                ||||||:::||||||
Db   1570  AATGCCCTCGGCATGGCCTTCGTGCAGAAGTACTTCTACATGACCGCCATATACTACAAGACA  1629

Qy    174  TyrThrAsnValAspGluPheGlyValAlaSerPheProAsnLysSerLeuSerPheThrThrGly    193
            ||||||          |||||            :::|||||||||::||
Db   1630  TACTTGTCGCTGGATGCCATCAACGCCAAAATATTTAACAAAATCGCCTTGGCGAAGCAC  1689

Qy    194  LeuPheGlyTrpGlyTyrLeuGlyLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeu    213
            ||         :::|||                :::|||||||::|||          |||
Db   1690  ATTCTGGGACCTTAAGATCAAAAAGGGCGTTGAGGAAGAATCGTCGAGCCAACAAGCCGAC  1749

Qy    214  AspIleGlyThrGlyThrProGlueHisIleThrSerSerTyrLysAsp    233
            :::||||||:::|||           :::||||||:::
Db   1750  GCGGCTC---CAAGGCAACGACGTCAAAAGCCATACCCCCTGGCCTACGGTTACAGG    1806

Qy    234  TyrMetAspThrGlnIleProAlaLeuProLysSerArgPheSerLeuMetVal    253
            ||||||          |||:::|||::||||||||||||||||||
Db   1807  TACAGGCCAGCCAAATCCCATACGCTTCCGTTCTCCGCTGGTC    1866

Qy    254  ValGlnArgLeuLeuAlaThrValAlaGlyThrTyrValAspThrTrpProTyrLysLysTrp    273
            |||                  ||:::||||||:::||||||||||||||||||:::||
Db   1867  GTCACCCGCTCTCGTGGACAACCTACCCGCCGGTTAAGCAACGACCGGTTGGCGTACAAGCCGTTGG  1926

Qy    274  TyrMetTyrLeuTyrAsnPheMetValAsnArgValPheIleProThrLysLysLysPhe    293
            ||:::||       |||:::||||||||||||||||||||||:::||:::
Db   1927  TTTGGAAAGGTGAAGAACCTCTTCACCGGTTAAGCAA------CCCAGCGAAAAGCCTAC    1980

Qy    294  AsnLysGluIleArgGluProSerLysSerAlaLeuLysGluLysValSerThrAspThrLys    313
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RESULT 30

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LOCUS       AF014757      575 bp    DNA        linear   INV 31-JAN-2001
DEFINITION  Babesia bigemina CGA rap-1 alpha (rap-1) gene, partial cds.
ACCESSION   AF014757
VERSION     AF014757.1  GI:2429255
KEYWORDS    .
SOURCE      Babesia bigemina.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
            loci of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
  MEDLINE   98135662
REFERENCE   2 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES             Location/Qualifiers
     source          1..575
                     /organism="Babesia bigemina"
                     /strain="CGA"
                     /db_xref="taxon:5866"
     gene            <1..>575
                     /gene="rap-1"
     CDS             <1..>575
                     /gene="rap-1"
                     /codon_start=2
                     /product="rap-1 alpha"
                     /protein_id="AAC47855.2"
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                     /translation="GVMSAEVVGDVSKTLLEANEVVNAEMEATQVNKDMQSQLSNVKE
                     TIVGEVCEKVAGNSTCGESVIAYVNCDEGDCLTLDSMKYKPLSLPNPYQLDAAFMLF
                     RESDSNPAKNEVKRFWMRSRSSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMT
                     TLYYKTYLTVDFTAAKFFNKLAFTTRLFGFG"
BASE COUNT      145 a    119 c    153 g    158 t
ORIGIN
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US-09-807-459-2 (1-458) x AF014757 (1-575)

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Alignment Scores:
  Pred. No.:
  Score:                 532.00       Length:        575
  Percent Similarity:    69.23%       Matches:       103
  Best Local Similarity: 52.82%       Conservative:   32
  Query Match:           22.55%       Mismatches:     52
  DB:                                 Indels:          8
                                      Gaps:            2
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Db  1981 ------GAAATTGACGAACCCATGCCACCGAGGAGGAG------------------ACCGAG 2019
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Qy   314 AspLeuPheGluAsnLysIleGlyGlnGlyThrValAlaSpPheAsnLysGluIleArg 333

Db  2020 CCTGTCGAGGAAAATAAG--------------------------TCAGTTTTTGGCAAG-- 2052
                |||||||                           |||    |||
Qy   334 AspProSerLysAlaLeuLysGluLysValSerAsn--------------------- 345

Db  2053 ------------GTCAGAGAAAAGCTTGGCAACATCCGCTTCAACACGGGGCATTTTC 2097
                         |||||||::::                 |||
Qy   346 AspAlaLys--------------------------- 348

Db  2098 CGAAAGGGTCAGGCAAAGACTTCGTCACTCCCACCTTTCCGAAGAGGACATTATGGGCAGC 2157
         :::                                                  |||
Qy   349 AspAlaLys----- 348

Db  2158 TTGTCGTCGTCGGCTGATGCCGTCGCTGTTGAGCCGGTGCTCGGAGTGTCATGGAG 2214
                                  AspLeuPheGluAsnLysIleGly
Qy   357 GlnGlyThrValAspPheThrIleAsnAsnGlnIleLeuArgAspProSerLysAlaLeuIleArg 376

Db  2215 GAACCTCAG----------AACGAGGAGGCAGGTGAACCCGAAGTGGGCGCCGGCTCCC 2262
         |||   ||||                    |||    |||
Qy   377 LysValSer-----------ThrGlyAlaGluAspLeu 385

Db  2263 AAGGCGCCTGAGAGTGAAAATGGGCGAAACTCGCAGACCAACTAGATGTTGCTTCAACTGTG 2322
                         AspLeuPheGluAsnLysIleGly
Qy   386 PheGluAsnLysIleGlyGln--------GlyThrValAspPhe 397

Db  2323 GCCTCAACCGAAAATGGGCGAAAGAGGAGTCTCTCGAAAGCTCCTAAAGGCACGCAGGATTTG 2382
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Qy   398 IleAsnAsnGlnIleLeuArgAsp-----------ProSerLysAlaLeuIle 410

Db  2383 ATGGACGAAGATGAGGAGCAGGAACCGAATTCTGACGAATTGCCTGCCAAGAGGAAGCGT 2442
         |||::|||                      |||||||
Qy   411 ArgLysValTyrThrGluAlaAlaSpAspLeuPheGluAsnLysIleGlyGlyGlyThrVal 430

Db  2443 AAAGCCTTCAAGCACAGGCTACAAAAAGTTCTTCAAGAACAATCTTGGACACCGGTGCAATT 2502
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Qy   431 AspPheIleAsnLysGluIleArgAspProSerLys 442

Db  2503 AAGGATGCCGCTACCGCATCGGGTTCCCGAAGAAG 2538
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RESULT 31

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LOCUS       AF014758      575 bp    DNA        linear   INV 31-JAN-2001
DEFINITION  Babesia bigemina CGP rap-1 alpha (rap-1) gene, partial cds.
ACCESSION   AF014758
VERSION     AF014758.1  GI:2429257
KEYWORDS    .
SOURCE      Babesia bigemina.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
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Qy     4 SerAspPserValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
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Db    14 GCAGAGGTGGTTGGAGATGTGTCCAAGACACCTTGCTGGAAGCCGCCAATGAAGTCGTCAA 73

Qy    24 AlaAlaAsnAlaTyrMetIleAlaAsnSerAspMetSerAspTyrLeuGluSerAlaValSerAsp 43
         |||||||||||||||||||||||||||||||||||||||||||:::    |||
Db    74 GAAATGCGAAGCAACTCAGGTCAACAAAGATATGCAAAGTCAATTGTCTAATGTTAAGGAG 133

Qy    44 AsnPheAlaGluArgIleCysSerSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
         :::||||||||||||||||||||||||||||||||||||||||||:::    |||
Db   134 ACCATTGTTGGTGAGGTCTGCGAGAAAGTTGCTGGGAAACTCTAACCTCGCGGTGAGACCGGTA 193

Qy    64 SerAlaTyrMetSerArgCysAlaLysGlnAsnAspCysLeuThrLeuGlnSerLeuTyr 83
         |||||||:::::|||||||||||||||||||||||||||||||||||||:::    |||
Db   194 ATTGCCTATGTTAACCCTTGTCAATGAGGGCGATTGTCTGACCCTTGACCGATG------ 247

Qy    84 ProLeuGluAlaLysTyrGlnProLeuThrLeuAspProThrTyrGlnLeuGluAlaAla 103
         :::::||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db   248 ----------AAGTACAAGCCGTTGAGTCTGCCAAATCCTTACCAGTTGGACCGGTGCC 295

Qy   104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGlyLysArgPheTrp 123
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Db   296 TTCATCCTTTTCAGGGAAAGTGATTCTAACCCTGCAAGAAATGCGCTTCTGG 355

Qy   124 MetArgPheArgArgGlyLysAsnHisSerTyrTyrPheHisAspHisHisPheAsnLeu 143
         |||||||||||||||      |||||||||||||||||||||||:::    |||
Db   356 ATGCGGTTCGAGG-----AGCAGCACGGCGACTACCATCACTTGTGTTGTTAGCTGTTG 409

Qy   144 GluLysAsnValThrArgAspAlaAspAlaThrAspTyrTrpIleGluAsnPheAlaSerArgTyr 163
         |||||||||||||||||||||||||||||||||||||||||||||||:::    |||
Db   410 AAGAAGAAATGTTGTACCGACGACCCTGAATCCAATGAGTTTGAGAACTTCGCATCGCACTAC 469

Qy   164 LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183
         |||||||||||||||||||||||||||||||||||||||||||||:::|||
Db   470 TTCTACACTGACTACGTTGTACTACAAGACTTACCTGACGTTGACTTTACGGCGGCTAAG 529

Qy   184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGly 198
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Db   530 TTCTTCAACAAGCTTGCTTTCACAACTCGCCTGTTCGGTTCGGT 574
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US-09-807-459-2 (1-458) x AF014758 (1-575)

Left column:

REFERENCE   1 (bases 1 to 575)
AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE   Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
            loci of Babesia bigemina
JOURNAL   Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
MEDLINE   98135662
REFERENCE   2 (bases 1 to 575)
AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES   Location/Qualifiers
     source   1..575
                     /organism="Babesia bigemina"
                     /strain="CGP"
                     /db_xref="taxon:5866"
     gene   <1..>575
                     /gene="rap-1"
     CDS   <1..>575
                     /gene="rap-1"
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                     /protein_id="AAC47860.2"
                     /db_xref="GI:1622027"
                     /translation="GVMSAEVVGDVSKTLLEANEVVNAEMEATQVNKDMQSOLSNVKE
                     TIVGEVCEKVAGNSTCGESVIAYVNRCDEGDCLTLDSMKYKPLSLPNPYQLDAAFMLF
                     RESDSNPAKNEVKRFWMRSRSSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMT
                     TLYKTYLTVDFTAAKFENKLAFTTRLFGFG"

BASE COUNT   145 a   119 c   153 g   158 t
ORIGIN

US-09-807-459-2 (1-458) x AF014758 (1-575)

Alignment Scores:
Pred. No.:
                    1.24e-34
Score: 532.00   Length: 575
Percent Similarity: 69.23%   Matches: 103
Best Local Similarity: 52.82%   Conservative: 32
Query Match: 22.55%   Mismatches: 52
DB: 3   Indels: 8
                                       Gaps: 2

Qy   4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
           :::::||| ||||||||||||||::|||:||||||::|||||||||||||||||| :::||
Db   4 GCAGAGGTGGTTGGAGATGTGTCCAAGACACCTTGCTGGAAGCCAATGAGGTTGTCAATGCT 73

Qy   24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
           |||| ||||:||||:||| ||||:||||::|| |||||||||||::|
Db   14 GCAGAGGTGGTTGGAGATGTGTCCAAGACACCTTGCTGGAAGCCAATGAGGTTGTCAATGCT 73

Qy   44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
           ::::||| ||| :|:||||||||:||| ||| ||||||||||| ||||
Db   74 GAAATGGAAGCAACTCAGGTCAACAAAGATATGCAAAGTCAATTGTCTAATGTTAAGGAG 133

Qy   64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
           |||||||||||:|||:|||:||:|||:|||||| ||| ||||||||||| :||
Db   134 ACCATTGTTGGTGAGGTCTGCGAGAAAGTTGCTGGAAACTCTACCTGCGGTGAGACGGTA 193

Qy   84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla 103
           ----------AAGTACAACGCCGTTGAGTCGTCGCCAAATCCTTACCAGTTGGACGTGCC 295

Qy   104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp 123
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Db   296 TTCATCCTTTTCAGGGAAAGTGATGTTAACCCTGCGAACAGCACCGGAAGCCGGTTCGG 355

Qy   124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisSerAspLeuValPheAsnLeu 143
           ||||:| || |||||| :||||||||||| |||||:|||
Db   356 ATGCGGTTCGAGG------AGCAGCCACAGGCGACTACCATCACTTTGTTGTTAGCTGTTG 409

Qy   144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163
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Db   410 AAGAAGAATGTTGTACCGACCCTGAATCCAATGATGTTGAGAACTTCGCATCGCAGTAC 469

Right column:

Qy   164 LeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183
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Qy   184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGly 198
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Db   530 TTCTTCAACAAGCTTGCTTTCACAACTCGCCTGTTCGGGTTCGGT 574

RESULT 32
LOCUS   AF014760   575 bp   DNA   linear   INV 31-JAN-2001
DEFINITION Babesia bigemina S1A rap-1 alpha (rap-1) gene, partial cds.
ACCESSION   AF014760
VERSION   AF014760.1 GI:2429261
KEYWORDS   .
SOURCE   Babesia bigemina.
  ORGANISM Babesia bigemina.
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 575)
AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE   Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
            loci of Babesia bigemina
JOURNAL   Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
MEDLINE   98135662
REFERENCE   2 (bases 1 to 575)
AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE   Direct Submission
JOURNAL   Submitted (16-JUL-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES   Location/Qualifiers
     source   1..575
                     /organism="Babesia bigemina"
                     /strain="S1A"
                     /db_xref="taxon:5866"
     gene   <1..>575
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     CDS   <1..>575
                     /gene="rap-1"
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                     /product="rap-1 alpha"
                     /protein_id="AAC47862.2"
                     /db_xref="GI:12622029"
                     /translation="GVMSAEVVGDVSKTLLEANEVVNAEMEATQVNKDMQSOLSNVKE
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                     RESDSNPAKNEVKRFWMRSRSSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMT
                     TLYKTYLTVDFTAAKFENKLAFTTRLFGFG"

BASE COUNT   145 a   119 c   153 g   158 t
ORIGIN

US-09-807-459-2 (1-458) x AF014760 (1-575)

Alignment Scores:
Pred. No.:
                    1.24e-34
Score: 532.00   Length: 575
Percent Similarity: 69.23%   Matches: 103
Best Local Similarity: 52.82%   Conservative: 32
Query Match: 22.55%   Mismatches: 52
DB: 3   Indels: 8
                                       Gaps: 2

Qy   4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSer 23
           :::::||| ||||||||||||||::|||:||||||::||||||||||||||||| :::||
Db   14 GCAGAGGTGGTTGGAGATGTGTCCAAGACACCTTGCTGGAAGCCAATGAGGTTGTCAATGCT 73

Qy   24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp 43
           ||| ||||:||||:||| ||||:||||::|| |||||||||||::|
Db   74 GAAATGGAAGCAACTCAGGTCAACAAAGATATGCAAAGTCAATTGTCTAATGTTAAGGAG 133

Qy   44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63
           ::::||| ||| :|:||||||||:||| ||| ||||||||||| ||||
Db   134 ACCATTGTTGGTGAGGTCTGCGAGAAAGTTGCTGGAAACTCTACCTGCGGTGAGACGGTA 193

Qy   64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83

RESULT 33

LOCUS   AF014762   575 bp   DNA   linear   INV 31-JAN-2001
DEFINITION   Babesia bigemina UYA rap-1 alpha (rap-1) gene, partial cds.
ACCESSION   AF014762
VERSION   AF014762.1 GI:2429265
KEYWORDS   .
SOURCE   Babesia bigemina.
  ORGANISM   Babesia bigemina
                Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
                Babesia.
REFERENCE   1 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE   Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
                loci of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
  MEDLINE   98135662
REFERENCE   2 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-1997) Department of Veterinary Microbiology and
                Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES   Location/Qualifiers
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                     /protein_id="AAC47864.2"
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                     RESDSNPARNEVKRFWMRSRSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMT
                     TLYYKTLYLTVDFTAAKFENKLAFTTRLFGFG"
BASE COUNT   145 a   119 c   153 g   158 t
ORIGIN

Alignment Scores:
Pred. No.:   1.24e-34
Score: 532.00
Percent Similarity: 69.23%

Length: 575
Matches: 103
Conservative: 32

US-09-807-459-2 (1-458) x AF014762 (1-575)

Qy   4   SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerVal   23
         ||||||| |||||||||||||||||||||||||||||||||||||||| :::
Db   14 GCAGAGGTGGTTGGGAGATGTGTCCAAGACCTTGCTGGAAGCCAATGAGGTTGTCAATGCT   73

Qy   24 AlaAlaAlaAsnAlaThrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp   43
Db   74 GAAATGGAAGCAACTCAGGTCAACAAAGATATGCAAAGTCAATTGTCTAATGTTAAGGAG   133

Qy   44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerSerAlaSerVal   63
Db   134 ACCATTGTTGGTAGAGTGTCTGCGAGAAAAGTTGCTGGGAAACTTCTTACCCTGCGGCGGGTAA   193

Qy   64 SerAlaThrTyrMetSerArgCysAlaLysGlnAspCysSerLeuThrLeuGlnSerLeuLysTyr   83
Db   194 ATTGGCTATGTTAACCGGTTGTGTGATGAGGCCGATTGTCTGACGCTTGACTTACGGCGGCTAAG   247

Qy   84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla   103
Db   248 ------------AAGTACAAGCCGTTGACTTTACCAGTTGACGCTGCC   295

Qy   104 PheIleLeuPheLysGluSerAspSerAsnProAlaAlaAsnSerThrGluLysArgPheTrp   123
Db   296 TTCATGCTTTTCAGGGAAAGTGATTCTAACCCTGCCGCAAATCCTTACCAGTTGACGCTGG   355

Qy   124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu   143
Db   356 ATGCGGTTCGAGG------AGCACGCCACGCGACTACCATCACTTTGTTGTTAGCTTGTTG   409

Qy   144 GluLysAsnValThrArgAspAlaAspValAlaSerArgTyr   163
Db   410 AAGAAGAATGTTGTACGCGACGCCCTGAATCCAATGAGTGTTGAGACTTCCGCATCGGCATAC   469

Qy   164 LeuTyrMetAlaThrLeuThrTyrTyrLysThrTyrThrAsnValAspGluProGlyTyrAlaSer   183
Db   470 TTCTACACATGACTACGGTTGTACTACACAAGACTTACCTGACGCTTTACGGCGGGCTAAG   529

Qy   184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTyrTrpGly   198
Db   530 TTCTTCAACAAGCTTTGCTTTCACAACTCGCCGTCGGTTTCGGT   574

RESULT 34

LOCUS   AF014768   575 bp   DNA   linear   INV 31-JAN-2001
DEFINITION   Babesia bigemina UYA rap-1 beta (rap-1) gene, partial cds.
ACCESSION   AF014768
VERSION   AF014768.1 GI:2429277
KEYWORDS   .
SOURCE   Babesia bigemina.
  ORGANISM   Babesia bigemina
                Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
                Babesia.
REFERENCE   1 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE   Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
                loci of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
  MEDLINE   98135662
REFERENCE   2 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-1997) Department of Veterinary Microbiology and
                Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES   Location/Qualifiers
     source   1..575
                     /organism="Babesia bigemina"
                     /strain="UYA"
                     /db_xref="taxon:5866"

Best Local Similarity: 52.82%
Query Match: 22.55%
DB: 3

Mismatches: 52
Indels: 8
Gaps: 2

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CDS             <1..>575
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                TLYYKTLTVDFTAAKFFNKLAFTTRLFGFG"

BASE COUNT     145 a     119 c     153 g     158 t
ORIGIN

US-09-807-459-2 (1-458) x AF014768 (1-575)

Alignment Scores:
Pred. No.:                1.24e-34
Score:                    532.00
Percent Similarity:       69.23%          Length:          575
Best Local Similarity:    52.82%          Matches:         103
Query Match:              22.55%          Conservative:     32
                                          Mismatches:       52
                                          Indels:            8
                                          Gaps:              2

Qy    4 SerAspSerValGlyAspValThrLysThrLeuLeuAlaAlaLeuAlaSerGluSerValAspSer  23
          ::::: ||| :|||||||||||||||||||||||
Db   14 GCAGAGGTGGTTGGGAGATGTGTCCAAGAACCTTGCTGGAAGCCAATGAGGTTGTCAATGCT  73

Qy   24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerArgAlaValSerAsp  43
          |||||| |||||
Db   74 GAAATGGAAGCAAACTCAGGTCAACAAAGAGATATGCAAAGTCAATTGTCTAAATGTTAAGGAG  133

Qy   44 AsnPheAlaGluArgIleCysSerSerGlnValProLeuThrLeuProAspProTyrGlnLeuGlu  63
          ||| |||||||
Db  134 ACCAATTGTTGGTGGAGGTCTCGCCAGAAAGTTCCAAATCCTTACCTCGGTGAGGCGTA  193

Qy   64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr  83
          ||||| |||||||
Db  194 ATTGCCTATGTTAACCGTTGTGATGAGGGCGAATTGTCTGACGCTTGACAGCAATG-----  247

Qy   84 ProLeuGluAlaLysTyrGlnLeuProLeuThrLeuProAspProTyrGlnLeuGluIleAlaAla  103
          ||||| |||||||
Db  248 -----AAGTACAACGCCGTTGAGTCTGCCCAAATCCTTACCAGTTGGACGCTGCC  295

Qy  104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGlyLysArgPheTrp  123
          |||:| ::||||||||
Db  296 TTCATCCTTTTCAGGGAAAGTGATGCTAACCCTGCGAAGAATGAGGTTGTCAATGCTGAAATGG  355

Qy  124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu  143
          |||||| ||
Db  356 ATGCGTTCGAGG------AGCAGCCACGGCGACTACCATCACTTTGTTGTTAGCTTGTTG  409

Qy  144 GluLysAsnValThrArgAspAlaAsplleGluAsnPheAlaSerArgTyr  163
          ::|||| ::|||
Db  410 AAGAAGAATGTTGTACGCGACCCTGAATCCAATGATGTTGAGAACTTCGCATCGCAGTAC  469

Qy  164 LeuTyrMetAlaThrLeuThrTyrIleLysThrGlyThrThrAsnValAspGluPheGlyAlaSer  183
          |||||:| |||
Db  470 TTCTACATGACTACGTTGTACTACAAGACTTTACCTACGGCGGGCTAAG  529

Qy  184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGly  198
          ||||| ::|||
Db  530 TTCTTCAACAAGCTTCGTTTCACAACTCGCCTGTTCGGTTCGGT  574
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RESULT 35
LOCUS       AF014761     575 bp     DNA     linear     INV 31-JAN-2001
DEFINITION  Babesia bigemina S2p rap-1 alpha (rap-1) gene, partial cds.
ACCESSION   AF014761
VERSION     AF014761.1  GI:2429263
KEYWORDS    .
SOURCE      Babesia bigemina.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
            loci of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
  MEDLINE   98135662
REFERENCE   2 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES             Location/Qualifiers
     source          1..575
                     /organism="Babesia bigemina"
                     /strain="S2p"
                     /db_xref="taxon:5866"
     gene            <1..>575
                     /gene="rap-1"
     CDS             <1..>575
                     /gene="rap-1"
                     /codon_start=2
                     /product="rap-1 alpha"
                     /protein_id="AAC47863.2"
                     /db_xref="GI:2622030"
                     /translation="GVMSAEVFGDVSKTLLEANEVVNAEMEATOVNKDMQSOLSNVKE
                     RESDSNPAKNEVKRFWMRSRSSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMT
                     TLYYKTLTVDFTAAKFFNKLAFTTRLFGFG"

BASE COUNT     145 a     119 c     152 g     159 t
ORIGIN

US-09-807-459-2 (1-458) x AF014761 (1-575)

Alignment Scores:
Pred. No.:                3.14e-34
Score:                    527.00
Percent Similarity:       69.11%          Length:          575
Best Local Similarity:    53.40%          Matches:         102
Query Match:              22.34%          Conservative:     30
                                          Mismatches:       51
                                          Indels:            8
                                          Gaps:              2

Qy    8 GlyAspValThrLysThrLeuLeuAlaAlaLeuAlaSerGluSerValAspSerAlaAlaAsnAla  27
          |||||||||||||||||||||||:| |||
Db   26 GGAGATGGTGTCCAAGAACCTTGCTGGAAGCCAATGAGGTTGTCAATGCTGAAATGGAAGCA  85

Qy   28 TyrMetIleAsnSerAspMetSerAspTyrLeuSerArgAlaValSerAspAsnPheAlaGlu  47
          :||| ::|||||||||||
Db   86 ACTCAGGTCAACAAAGAGATATGCAAAGTCAATTGTCTAAATGTTAAGGAGACCAATTGTTGGT  145

Qy   48 ArgIleCysSerSerGlnValProLeuGlyLysAsnCysSerSerAlaSerValSerAlaTyrMet  67
          ::||| |:|
Db  146 GAGGTCTCGCCAGAAAGTTCCTGGAAACTCTACCTCGGTGAGGCGTAATTGCCTATGTT  205

Qy   68 SerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyrProLeuGluAla  87
          |||||||||||| ||
Db  206 AACCGTTGTGATGAGGGCGAATTGTCTGACGCTTGACAGCAATG-----------  247

Qy   88 LysTyrGlnLeuProLeuThrLeuProAspProTyrGlnLeuGluIleAlaAlaPheIleLeuPhe  107
          ||||| |||||||
Db  248 AAGTACAACGCCGTTGAGTCTGCCCAAATCCTTACCAGTTGGACGCTGCCTTCATCGTTTTC  307

Qy  108 LysGluSerAspAlaAsnProAlaAsnSerThrGlyLysArgPheTrpMetArgPheArg  127
          ::|||||||||||||||||||||||||||||| :::
Db  308 AGGGAAAGTGATTCTAACCCTGCGAAGAATGAGGTTGAACGGCTTCGGATGCGTTCGAGG  367

Qy  128 ArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuGluLysAsnVal  147
          |||:| :::|||
Db  368 -----AGCAGCCACGGCGACTACCATCACTTTGTTGTTAGCTTGTTGGAAGAAGAATGTT  421

Qy  148 ThrArgAspAlaAspIleGluAsnPheAlaSerArgTyrLeuTyrMetAla  167
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RESULT 36

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Db  422 GTACGCGACCCTGAATCCAATGATGTTGAGAACTTCGCATCGCAGTACTTCTACATGACT 481
        |||||  :::::||||||||  |:||||||::||||||||  ||||  ||  ||  |||||
Qy  168 ThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSerPhePheAsnLys 187

Db  482 ACGGTTGTACTACAACAGACTTACCTGACGCGGCGGCCTAAGTTCTTCAACAG 541
        |||  ||  ||||||||  ||||||||||||  |||  |||||||||||||||
Qy  188 LeuSerPheThrThrGlyLeuPheGlyTrpGly 198

Db  542 CTTGCTTCACAAACTCGCCTGTTCGGTTTCGGT 574
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LOCUS       AF014767                 575 bp    DNA     linear   INV 31-JAN-2001
DEFINITION  Babesia bigemina S2P rap-1 beta (rap-1) gene, partial cds.
ACCESSION   AF014767
VERSION     AF014767.1  GI:2429275
KEYWORDS    .
SOURCE      Babesia bigemina.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
            loci of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
  MEDLINE   98135662
REFERENCE   2 (bases 1 to 575)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES             Location/Qualifiers
     source          1..575
                     /organism="Babesia bigemina"
                     /strain="S2P"
                     /db_xref="taxon:5866"
     gene            <1..>575
                     /gene="rap-1"
     CDS             <1..>575
                     /gene="rap-1"
                     /codon_start=2
                     /product="rap-1 beta"
                     /protein_id="AAC47869.2"
                     /db_xref="GI:12622036"
                     /translation="GVMSAEVFGDVSKTLLEANEVVNAEMEATQVNKDMQSQLSNVKE
                     RESDSNPAKNEVKRFWMRSRSSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMT
                     TLYYKTYLIVDFTAAKFFNKLAFTTRLFGFG"
BASE COUNT      145 a    119 c    152 g    159 t
ORIGIN
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Alignment Scores:

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Pred. No.:
Score:                    3.14e-34
Score:                    527.00
Percent Similarity:       69.11%
Best Local Similarity:    53.40%
Query Match:              22.34%
DB:                       3
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US-09-807-459-2 (1-458) x AF014767 (1-575)

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                Length:        575
                Matches:       102
                Conservative:  30
                Mismatches:    51
                Indels:        8
                Gaps:          2

Qy    8 GlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSerAlaAlaAsnAla 27
        ||||||||||||  :::||  ||  ||:|||  :||  ::::
Db   26 GGAGATGTCCAAGACNCCTTGCTGGAAGCCAATCAGGTTGTCAATGCTGAAATGCAAGCA 85

Qy   28 TyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAlaSerAspAsnPhe 47
        :::|||  ||||||  ::|       ||||  :||
Db   86 ACTCAGGTCAACAAAGATATGCAAAGTCAATTGTCTAATGTTAAGGAGAGACCATTGTGGT 145

Qy   48 ArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerValSerAlaThrTyrMet 67
        :::|||.  .::|||.  ::||||||
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RESULT 37

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Db  146 GAGGTCTGCGAGAAAGTTGCTCGGAAACTCACCTGCGGTGAGACGGTAAATGCCTATGTT 205
        |||  ||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Qy   68 SerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyrProLeuGluAla 87

Db  206 AACCGTTGTGATGAGGGCGATTGTCTGACGGCTTGACACAGTG------ 247
        |||  ||  |||||||  ||||  :||||||  |||  ||||
Qy   88 LysTyrCysGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAlaPheIleLeuPhe 107

Db  248 AAGTACAAGCCCGTTGAGTCTGCCCAAATCCTTACACAGTTGGACGCGCCTGCCTTCATGCTTTTC 307
        |||||||||  :::|||||  :::|||||||||||||||  ::|||||  :::|||||||||:::|
Qy  108 LysGluSerAspAlaAsnProLeuAlaAsnSerThrGlyLysArgPheTrpMetArgPheArg 127

Db  308 AGGGAAAGTGATTCTAACCCTGCGAAGAATGAGGTGAAGCGGTTCTGGATGCGGTTCCGAGG 367
        |||  :::|||  ||  :::|||||||||||||||||||||||||||||||  |||  |||||
Qy  128 ArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuGluLysAsnVal 147

Db  368 ------AGCAGGCCACGGCGACTACCATCACGTTGGTTCGATCTTGTTGAAGAAGAATGTT 421
               :::|||||  |||  ||||  |||||||||||  ||||  :::|||||||||||||
Qy  148 ThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyrLeuThrTyrMetAla 167

Db  422 GTACGCGACCCTGAATCCAATGATGTTGAGAACTTCGCATCGCAGTACTTCTACATGACT 481
        |||||  :::::||||||||  |:||||||::||||||||  ||||  ||  ||  |||||
Qy  168 ThrLeuTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSerPhePheAsnLys 187

Db  482 ACGGTTGTACTACAACAGACTTACCTGACGCGGCGGCCTAAGTTCTTCAACAG 541
        |||  ||  ||||||||  ||||||||||||  |||  |||||||||||||||
Qy  188 LeuSerPheThrThrGlyLeuPheGlyTrpGly 198

Db  542 CTTGCTTCACAAACTCGCCTGTTCGGTTTCGGT 574
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LOCUS       AF014764                 574 bp    DNA     linear   INV 31-JAN-2001
DEFINITION  Babesia bigemina CGP rap-1 beta (rap-1) gene, partial cds.
ACCESSION   AF014764
VERSION     AF014764.1  GI:2429269
KEYWORDS    .
SOURCE      Babesia bigemina.
  ORGANISM  Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 574)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
            loci of Babesia bigemina
  JOURNAL   Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
  MEDLINE   98135662
REFERENCE   2 (bases 1 to 574)
  AUTHORS   Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES             Location/Qualifiers
     source          1..574
                     /organism="Babesia bigemina"
                     /strain="CGP"
                     /db_xref="taxon:5866"
     gene            <1..>574
                     /gene="rap-1"
     CDS             <1..>574
                     /gene="rap-1"
                     /codon_start=1
                     /product="rap-1 beta"
                     /protein_id="AAC47866.2"
                     /db_xref="GI:12622033"
                     /translation="GCYVSRVGDVSKTLLAANEVVNAEMEAAQINEDMKIQLANVKE
                     TIVDEVCRKDAGSPTCRKSVTAYVDRCEDGDCLTLDSMKYKPLSLPNYQLDAAFMLF
                     RESDSNPAKNEVKRFWMRSRSSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMT
                     TLYYKTYLIVDFTAAKFFNKLAFTTRLFGFG"
BASE COUNT      142 a    124 c    156 g    152 t
ORIGIN
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Alignment Scores:

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Pred. No.:                          1.15e-33      Length:              574
Score:                              520.00        Matches:             102
Percent Similarity:                 58.75%        Conservative:         30
Best Local Similarity:              53.12%        Mismatches:           52
Query Match:                        22.04%        Indels:                8
DB:                                 3             Gaps:                  2
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US-09-807-459-2 (1-458) x AF014764 (1-574)

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Qy      7  ValGlyAspValThrLysThrLeuLeuAlaAlaSerGluSerValAspSerAlaAlaAsn  26
           |||   ||||:||
Db     22  GTTGGAGATGTGTCCAAGACCTTGCTAGCCAGCCAAGCGAGGTTGTCAATGCTGAAATGGAA  81

Qy     27  AlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAspAsnPheAla  46
           ||||||                  ||     ||:::
Db     82  GCAGCTCAGATATTAACGAAGATATGAAGAGATTCAGTTGGGCGAACGTCAAGGAGACCATCGTT  141

Qy     47  GluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerValSerAlaThrTyr  66
           :::|||     ||:|||
Db    142  GATGAGGTCTCCAGAAAAAGATGCTGGAAGCCCTACGTGCCCCAAGAGACCGTAATTGCCTAT  201

Qy     67  MetSerArgCysAlaLysGlnAspCysLeuThrLeuLysThrTyrProLeuGlu  86
           :::                |||||||
Db    202  GTTGACCGTTGTGATGAGGGGCCGATTGGTCTGACGGCTTGACACAGCATG-----------  246

Qy     87  AlaLysThrArgGlnProLeuThrLeuProAspProTyrGlnLeuGlnAlaAlaAlaPheIleLeu  106
           |||||:::||||||:::                         :::||||||||:::|||
Db    247  ---AAGTACAAGACCGTTGAGTGTCGTCCAAATCCTTACCAGTTGGACCCTGCCTTCATCGTT  303

Qy    107  PheLysGluSerArgAspAlaAsnProAlaAsnSerThrGlyLeuLysArgPheTrpMetArgPhe  126
           |||||||   |||:::||||||
Db    304  TTCAGGGAAAGTGAATTCAACCCTGCCGAAGAATGCAAGCGCTTCTGGATGCGTTCG  363

Qy    127  ArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuGluLysAsn  146
           |||||||
Db    364  AGG-----------AGCAGCCACGGCGACTACCATCACTTTGTTGTTGAGAAGAAT  417

Qy    147  ValThrArgAspAlaAspAlaThrArgIleGluAsnPheAlaSerArgArgTyrLeuThrTyrMet  166
           |||||||
Db    418  GTTGTACGGCAGACCGTGAATCAAATGACATGGAACTCGAGTACTTCTACATG  477

Qy    167  AlaThrLeuTyrTyrTyrTyrTyrArgThrAsnValAspGluPheGlyAlaSerPhePheAsn  186
           ||||||                    |||    ||:::    |||||||
Db    478  ACTACGTTGTACTACAGACTTACCTGACCCGTGTGATGAGGGCGGATTGTCTGACGCTTGACAGCATG-----  537

Qy    187  LysLeuSerPheThrThrArgGlyLeuPheGlyTrpGly  198
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Db    538  AAGCTTGCTTTCACAACTCGCCCTGTTGTTCGGT  573
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BASE COUNT   202 a   173 c   208 g   240 t

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/organism="Babesia bigemina"
/strain="PTR"
/db_xref="taxon:5866"

gene   166..>823
          /gene="rap-1"

CDS   166..>823
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          /product="rap-1 alpha"
          /protein_id="AAC47861.2"
          /db_xref="GI:12622028"
          /translation="MRSFLGVCRGALLLVARSGSSAIRYTHRSGVMSAEVVGDVSKTLL
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          DCLFTLDSMKVKPLSLPNPYQLDDAAFMLFRESDSNPAKNEVKCFWMMRSRSSHGDYHHFV
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Alignment Scores:
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Pred. No.:                          1.78e-33      Length:              823
Score:                              520.00        Matches:             101
Percent Similarity:                 58.72%        Conservative:         33
Best Local Similarity:              51.79%        Mismatches:           53
Query Match:                        22.04%        Indels:                8
DB:                                 3             Gaps:                  2
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US-09-807-459-2 (1-458) x AF014759 (1-823)

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Qy      4  SerAspSerValGlyAspValThrLysThrLeuLeuLeuAlaAlaSerGluSerValAspSer  23
           :::::                |||||||:::
Db    262  GCAGAGGTGGTGGGAGATGTGTCCAAGACCTTGGAAGCCACCAAGAGAGGTTGTCAAATGCT  321

Qy     24  AlaAlaAsnAlaAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp  43
           :::                |||          |||:::
Db    322  GAAATGGAGCAACTCACGGTCAACAAAGATATACAAAGTCAATTGTCTAATGTGAAGGAG  381

Qy     44  AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal  63
           :::                |||          :::
Db    382  ACCATCGTTGATGAGGTCTGCAGAAAAGATGCTGGAAACTTCTACCTGCCGGAGAATGCA  441

Qy     64  SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr  83
           |||    ||:::
Db    442  ATTGCCTATGTTAACCGTGTGATGAGGGCGGATTGTCTGACGCTTGACAGCATG-----  495

Qy     84  ProLeuGluAlaLysThrArgGlnProLeuThrLeuProAspProTyrGlnLeuGlnAlaAla  103
           |||
Db    496  ------AAGTACAAGACCGTTGAGTGTCGTCCAAATCCTTACCAGTTGGACCCTGCC  543

Qy    104  PheIleLeuPheLysGluSerArgAspAlaAsnProAlaAsnSerThrGlyLeuLysArgPheTrp  123
           |||:::||||||:::                      :::            |||||||
Db    544  TTCATCGTTTTCAGGGAAAGTGAATTCAACCCTGCCGAAGAATGCAAGCGCTTCTGG  603

Qy    124  MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuGluLeu  143
           |||||||                                      :::|||
Db    604  ATGCGTTCGAGG-----------AGCAGCCACGGCGACTACCATCACTTTGTTGTTG  657

Qy    144  GluLysAsnValThrArgAspAlaAspAlaThrArgIleGluAsnPheAlaSerArgArgTyr  163
           :::::::                |||||||:::
Db    658  AAGAAGAAATGTTGTACGGCGAGACCGTGAATCAAATGACATGGAACTCGGATCCGATGAC  717

Qy    164  LeuThrTyrMetAlaThrLeuTyrTyrTyrTyrArgThrAsnValAspGluPheGlyAlaSer  183
           |||||||                ||||||||                 |||
Db    718  TTCTACAATGACTACGTTGTACTACAGACTTACCTGACCCGTGTGATGAGGGCGGCTAAG  777

Qy    184  PhePheAsnLysLeuSerPheThrThrArgGlyLeuPheGlyTrpGly  198
           |||||||                |||||||:::||:::||||||
Db    778  TTCTTCAACAAGCTTGCTTTCACAACTCGCCCTGTTGTTCGGTTTCG  822
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ACCESSION   AF014763
VERSION     AF014763.1  GI:2492267
KEYWORDS    .
SOURCE      Babesia bigemina.
ORGANISM    Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 575)
AUTHORS     Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE       Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
            loci of Babesia bigemina
JOURNAL     Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
MEDLINE     98135662
REFERENCE   2 (bases 1 to 575)
AUTHORS     Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES             Location/Qualifiers
     source          1..575
                     /organism="Babesia bigemina"
                     /strain="CGA"
                     /db_xref="taxon:5866"
     gene            <1..>575
                     /gene="rap-1"
     CDS             <1..>575
                     /gene="rap-1"
                     /codon_start=2
                     /product="rap-1 alpha"
                     /protein_id="AAC47865.2"
                     /db_xref="GI:1262032"
                     /translation="GVMSAEVGVGDVSKTLLAANEVVNAEMEAAQINEDMKIQLANVKE
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                     RESDSNPAKNEVKCFWMRSRSSHGDYHHPFVSLLKKNVVRDPESNDVENFASQYFYMT
                     TLIYKTYLTIVDFTAAKFFNKLAFTTRLFGFG"
BASE COUNT     144 a    123 c    156 g    152 t
ORIGIN
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US-09-807-459-2 (1-458) x AF014763 (1-575)

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Alignment Scores:
Pred. No.:               3
Score:                   4.25e-33            Length:          575
Percent Similarity:      68.21%              Matches:         101
Best Local Similarity:   51.79%              Conservative:     32
Query Match:             21.75%              Mismatches:       54
DB:                                          Indels:            8
                                             Gaps:              2

Qy    4 SerAspSerValGlyAspValThrIleCysSerGlnValProLysGlySerAsnCysSerAlaAspSerVal  23
          :::    :::|||      :::|||:::         |||      :::|||
Db   14 GCAGAGGTGGTTGGAGATGTGTCCAAGACCTTGCTGGCAGCCAACGAGGTTGTCAATGCT           73

Qy   24 AlaAlaAsnAlaTyrMetIleAsnSerAspMetSerAspTyrLeuSerAlaValSerAsp            43
Db   74 GAAATGGAAGCAGCTCAGATAAACGAAGATATGAAGATTCAGTTGGCAAACGTCAAGGAG          133

Qy   44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal            63
Db  134 ACCATCGTTGATGAGGTCTGCAGAAAAGATGCTGGAAGCCCTACGTGCCGCAAGAGCGTA          193

Qy   64 SerAlaTyrMetSerArgCysValAlaLysGlyAspCysLeuThrLeuGlnSerLeuLysTyr          83
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Qy   84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProAspProTyrGlnLeuGluAlaAla           103
Db  248 ------------AAGTACAAGCCGTTGAGTCTGCCAAATCCTTACCAGTTGGACGCTGCC          295

Qy  104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp           123
Db  296 TTCAACGTTTTCACGGAAAAGTGATTCTAACCCTCGCGAAGAAGTGATGAGGTGAAGTGCTTCTCG    355

Qy  124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu           143
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RESULT 40
LOCUS       AF014765                 866 bp    DNA     linear   INV 31-JAN-2001
DEFINITION  Babesia bigemina PTR rap-1 beta (rap-1) gene, partial cds.
ACCESSION   AF014765
VERSION     AF014765.1  GI:2429271
KEYWORDS    .
SOURCE      Babesia bigemina.
ORGANISM    Babesia bigemina
            Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae;
            Babesia.
REFERENCE   1 (bases 1 to 866)
AUTHORS     Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE       Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
            loci of Babesia bigemina
JOURNAL     Mol. Biochem. Parasitol. 90 (2), 479-489 (1997)
MEDLINE     98135662
REFERENCE   2 (bases 1 to 866)
AUTHORS     Hotzel,I., Suarez,C.E., McElwain,T.F. and Palmer,G.H.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-1997) Department of Veterinary Microbiology and
            Pathology, Washington State University, Pullman, WA 99164-7040, USA
FEATURES             Location/Qualifiers
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     CDS             209..>866
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                     AANEVVNAEMEAAQINEDMKIQLANVKETIVDEVCRKDAGSPTCRKSVIAYVDRCDEG
                     DCLTLDSMKYKPLSLPNYQLDDAAFMLFRESDSNPAKNEVKCFWMRSRSSHGDYHHPFV
                     VSLLKKNVVRDPESNDVENFASQYFYMTTLIYKTYLTIVDFTAAKFFNKLAFTTRLFGF
                     G"
BASE COUNT     208 a    184 c    227 g    247 t
ORIGIN
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US-09-807-459-2 (1-458) x AF014765 (1-866)

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Alignment Scores:
Pred. No.:               4
Score:                   6.98e-33            Length:          866
Percent Similarity:      68.21%              Matches:         101
Best Local Similarity:   51.79%              Conservative:     32
Query Match:             21.75%              Mismatches:       54
DB:                                          Indels:            8
                                             Gaps:              2

Qy    4 SerAspSerValGlyAspValThrIleCysSerGlnValProLysGlySerAsnCysSerAlaAspSer   23
Db    4 SerAspSerValGlyAspValThrIleLeuLeuAlaAlaSerGluSerValAspSer              23

Db  356 ATGCGTTCGAGG------AGCAGCCACGGCGACGACTACCAATCACTTGTTGTTGAGCTTGTTG       409

Qy  144 GluLysAsnValThrArgSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTyr           163
          |||   |||||||     :::|||   :::|||   |||:::      |||
Db  410 AAGAAGAATGTTGTACCGCAGACCCTGAATCCAATGAATGATGTTGAGAACTTCGCATCGCAGTAC    469

Qy  164 LeuThrTyrMetAlaThrLeuTyrTyrLysThrTyrArgAsnValAspGlyTrpGlyAlaSer       183
          :::   |||   |||   :::         |||         :::|||
Db  470 TTCTACACATGACTACGTTGTACTACACAAGACTTACCTGACCGTTGACGTTGACACCGTCGGTAAG  529

Qy  184 PhePheAsnLysLeuSerPheThrThrGlyLeuPheGlyTrpGly                         198
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Db  530 TTCTTCAACAAGCCTTGCTTTTCACAACTCGCCTCGTTCGGTTCGGT                       574
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Db  365 GAAATGGGAAGCAGCAGCTTCAGATTAACGAAGAGATATGAAGAGATTCAGTTGGCGAACGTCAAGGAG 424
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Qy   44 AsnPheAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerSerAlaSerVal 63
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Db  425 ACCATCGTTGATGAGGTCTCTGCAGAAAAAGATGCTGGAAGCCCTACGTGCCCGCAAGAGCGTA 484

Qy   64 SerAlaTyrMetSerArgCysAlaLysGlnAspCysLeuThrLeuGlnSerLeuLysTyr 83
            ||||||                       ||:::
Db  485 ATTTGCCTACGTTGACCGGTTGTTGATGAGGGGGGATTGTTCTGACGGTGACAGCATG------ 538

Qy   84 ProLeuGluAlaLysTyrGlnProLeuThrLeuProCysAspProTyrGlnLeuGluAlaAla 103
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Db  539 ------------AAGTACAAGCCGTTGAGTCTGCCAAATCCTTACCAGTTGGACGGCTGCC 586

Qy  104 PheIleLeuPheLysGluSerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrp 123
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Qy  124 MetArgPheArgGlyLysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeu 143
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Qy  144 GluLysAsnValThrArgAspAlaAspAlaThrAspIleGluAsnPheAlaSerArgTyr 163
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Db  701 AAGAAGAATGTTGTACGGCGACCCTGAATCCAATGATGTTGAGAACTTCGCAATCCGACGTAC 760

Qy  164 LeuTyrMetAlaThrLeuThrTyrTyrLysThrTyrThrAsnValAspGluPheGlyAlaSer 183
            |||
Db  761 TTCTACATGACTACCGTTGTTACTACAAGACTTACCTGACCGTTACGGCGGGCTAAG 820

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